```
   1 CCATTCCAAA CAAGTCAGGA AAGCCTGCAC AGGACTGGAT AAATAATTAA
  51 GAACAGAGTG TTCTGAACAT CAACACAAAG TGGAAGAACC TTAAGCTGAA
 101 GGTACAGTAT ATTATTTACA CTGAAGGGGC TTGTGTGTGG ACAAGAAAGC
 151 GCTGACAGCT CAAATGGATC CCATGGAACT GAGAAATGTC AACATCGAAC
 201 CAGATGATGA GAGCAGCAGT GGAGAAAGTG CTCCAGATAG CTACATCAGG
 251 ATAGGAAATT CAGAAAAGGC AGCAATGAGC AGTCAATTTG CTAATGAAGA
 301 CACTGAAAGT CAGAAATTCC TGACAAATGG ATTTTTGGGG AAAAAGAAGC
 351 TGGCAGATTA TGCTGATGAA CACCATCCCG GAACCACTTC CTTTGGAATG
 401 TCTTCATTTA ACCTGAGTAA TGCCATCATG GGCAGTGGGA TCCTGGGCTT
 451 GTCCTATGCC ATGGCCTACA CAGGGGTCAT ACTTTTTATA ATCATGCTGC
 501 TTGCTGTGGC AATATTATCA CTGTATTCAG TTCACCTTTT ATTAAAAACA
 551 GCCAAGGAAG GAGGGTCTTT GATTTATGAA AAATTAGGAG AAAAGGCATT
 601 TGGATGGCCG GGAAAAATTG GAGCTTTTGT TTCCATTACA ATGCAGAACA
 651 TTGGAGCAAT GTCAAGCTAC CTCTTTATCA TTAAATATGA ACTACCTGAA
 701 GTAATCAGAG CATTCATGGG ACTTGAAGAA AATACTGGAG AATGGTACCT
 751 CAATGGCAAC TACCTCATCA TATTTGTGTC TGTTGGAATT ATTCTTCCAC
 801 TTTCGCTCCT TAAAAATTTA GGTTATCTTG GCTATACCAG TGGATTTTCT
 851 CTTACCTGCA TGGTGTTTTT TGTTAGTGTG GTGATTTACA AGAAATTCCA
 901 AATACCCTGC CCTCTACCTG TTTTGGATCA CAGTGTTGGA AATCTGTCAT
 951 TCAACAACAC GCTTCCAATG CATGTGGTAA TGTTACCCAA CAACTCTGAG
1001 AGTTCTGATG TGAACTTCAT GATGGATTAC ACCCACCGCA ATCCTGCAGG
1051 GCTGGATGAG AACCAGGCCA AGGGCTCTCT TCATGACAGT GGAGTAGAAT
1101 ATGAAGCTCA TAGTGATGAC AAGTGTGAAC CCAAATACTT TGTATTCAAC
1151 TCCCGGACGG CCTATGCAAT TCCTATCCTA GTATTTGCTT TTGTATGCCA
1201 CCCTGAGGTC CTTCCCATCT ACAGTGAACT TAAAGATCGG TCCCGGAGAA
1251 AAATGCAAAC GGTGTCAAAT ATTTCCATCA CGGGGATGCT TGTCATGTAC
1301 CTGCTTGCCG CCCTCTTTGG TTACCTAACC TTCTATGGAG AAGTTGAAGA
1351 TGAATTACTT CATGCCTACA GCAAAGTGTA TACATTAGAC ATCCCTCTTC
1401 TCATGGTTCG CCTGGCAGTC CTTGTGGCAG TAACACAAAC TGTGCCCATT
1451 GTCCTCTTCC CAATTCGTAC ATCAGTGATC ACACTGTTAT TTCCCAAACG
1501 ACCCTTCAGC TGGATACGAC ATTTCCTGAT TGCAGCTGTG CTTATTGCAC
1551 TTAATAATGT TCTGGTCATC CTTGTGCCAA CTATAAAATA CATCTTCGGA
1601 TTCATAGGGG CTTCTTCTGC CACTATGCTG ATTTTTATTC TTCCAGCAGT
1651 TTTTTATCTT AAACTTGTCA AGAAAGAAAC TTTTAGGTCA CCCCAAAAGG
1701 TCGGGGCTTT AATTTTCCTT GTGGTTGGAA TATTCTTCAT GATTGGAAGC
1751 ATGGCACTCA TTATAATTGA CTGGATTTAT GATCCTCCAA ATTCCAAGCA
1801 TCACTAACAC AAGGAAAAAT AC
```

FEATURES:

```
5'UTR:        1-163
Start Codon: 164
Stop Codon:  1805
3'UTR:        1808
```

FIGURE 1, page 1 of 2

HOMOLOGOUS PROTEINS:

Top BLAST Hits:

	Score	E
CRA|145000039337444 /altid=gi|12017941 /def=gb|AAG45335.1|AF295...	975	0.0
CRA|114000033649823 /altid=gi|10945621 /def=gb|AAG24618.1|AF298...	597	e-169
CRA|160000003782430 /altid=gi|8677401 /def=gb|AAF75589.2|AF1736...	591	e-168
CRA|148000002720069 /altid=gi|8248427 /def=gb|AAF74195.1|AF2496...	587	e-166
CRA|87000000006802 /altid=gi|7243145 /def=dbj|BAA92620.1| (AB03...	578	e-164
CRA|18000005069115 /altid=gi|5870893 /def=ref|NP_006832.1| tran...	500	e-140
CRA|88000001154721 /altid=gi|7406950 /def=gb|AAF61849.1|AF15985...	496	e-139
CRA|66000019404613 /altid=gi|9506837 /def=ref|NP_061849.1| amin...	495	e-139
CRA|100000004435450 /altid=gi|8926332 /def=gb|AAF81797.1|AF2730...	492	e-138
CRA|335001098689635 /altid=gi|11434147 /def=ref|XP_006635.1| hy...	480	e-134

EST:

	Score	E
gi|10934204 /dataset=dbest /taxon=96...	1072	0.0
gi|10286121 /dataset=dbest /taxon=96...	718	0.0
gi|9872634 /dataset=dbest /taxon=960...	680	0.0
gi|2656674 /dataset=dbest /taxon=9606 ...	549	e-154
gi|9882497 /dataset=dbest /taxon=960...	541	e-151
gi|689641 /dataset=dbest /taxon=9606 /...	525	e-147

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

Expression information from BLAST dbEST hits:

gi|10934204 Whole embryo (mainly head)

gi|10286121 Hepatocellular carcinoma

gi|9872634 Non-cancerous liver

gi|2656674 Fetal liver spleen

gi|9882497 Non cancerous liver

gi|689641 Liver

Expression information from PCR-based tissue screening panels:

Mixed tissue (Brain, Heart, Kidney, Lung, Spleen, Testis, Leukocyte)

FIGURE 1, page 2 of 2

```
  1 MDPMELRNVN IEPDDESSSG ESAPDSYIRI GNSEKAAMSS QFANEDTESQ
 51 KFLTNGFLGK KKLADYADEH HPGTTSFGMS SFNLSNAIMG SGILGLSYAM
101 AYTGVILFII MLLAVAILSL YSVHLLLKTA KEGGSLIYEK LGEKAFGWPG
151 KIGAFVSITM QNIGAMSSYL FIIKYELPEV IRAFMGLEEN TGEWYLNGNY
201 LIIFVSVGII LPLSLLKNLG YLGYTSGFSL TCMVFFVSVV IYKKFQIPCP
251 LPVLDHSVGN LSFNNTLPMH VVMLPNNSES SDVNFMMDYT HRNPAGLDEN
301 QAKGSLHDSG VEYEAHSDDK CEPKYFVFNS RTAYAIPILV FAFVCHPEVL
351 PIYSELKDRS RRKMQTVSNI SITGMLVMYL LAALFGYLTF YGEVEDELLH
401 AYSKVYTLDI PLLMVRLAVL VAVTQTVPIV LFPIRTSVIT LLFPKRPFSW
451 IRHFLIAAVL IALNNVLVIL VPTIKYIFGF IGASSATMLI FILPAVFYLK
501 LVKKETFRSP QKVGALIFLV VGIFFMIGSM ALIIIDWIYD PPNSKHH
```

FEATURES:
Functional domains and key regions:
[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

Number of matches: 5
```
      1       83-86 NLSN
      2     260-263 NLSF
      3     264-267 NNTL
      4     276-279 NNSE
      5     369-372 NISI
```

[2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE
cAMP- and cGMP-dependent protein kinase phosphorylation site

```
        503-506 KKET
```

[3] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 7
```
      1       33-35 SEK
      2       49-51 SQK
      3     129-131 TAK
      4     290-292 THR
      5     360-362 SRR
      6     473-475 TIK
      7     506-508 TFR
```

[4] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 5
```
      1       18-21 SSGE
      2       22-25 SAPD
      3     129-132 TAKE
      4     305-308 SLHD
      5     309-312 SGVE
```

FIGURE 2, page 1 of 4

```
[5] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 6
     1     95-100 GLSYAM
     2    153-158 GAFVSI
     3    164-169 GAMSSY
     4    186-191 GLEENT
     5    296-301 GLDENQ
     6    482-487 GASSAT

[6] PDOC00009 PS00009 AMIDATION
Amidation site

          58-61 LGKK
```

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	79	99	1.125	Certain
2	102	122	2.503	Certain
3	153	173	1.197	Certain
4	197	217	1.785	Certain
5	222	242	2.123	Certain
6	332	352	1.240	Certain
7	370	390	2.166	Certain
8	414	434	1.301	Certain
9	453	473	1.520	Certain
10	476	496	2.166	Certain
11	515	535	2.628	Certain

FIGURE 2, page 2 of 4

BLAST Alignment to Top Hit:
>CRA|145000039337444 /altid=gi|12017941
          /def=gb|AAG45335.1|AF295535_1 (AF295535) amino acid
          transport system A3 [Rattus norvegicus] /org=Rattus
          norvegicus /taxon=10116 /dataset=nraa /length=547
          Length = 547

  Score = 975 bits (2492), Expect = 0.0
  Identities = 478/547 (87%), Positives = 508/547 (92%)

Query: 1   MDPMELRNVNIEPDDESSSGESAPDSYIRIGNSEKAAMSSQFANEDTESQKFLTNGFLGK 60
             MDP+ELR+VNIEP ++S S +S   Y +GNSEK AM SQFANED ESQKFLTNGFLGK
Sbjct: 1   MDPIELRSVNIEPYEDSCSVDSIQSCYTGMGNSEKGAMDSQFANEDAESQKFLTNGFLGK 60

Query: 61   KKLADYADEHHPGTTSFGMSSFNLSNAIMGSGILGLSYAMAYTGVILFIIMLLAVAILSL 120
             K L DYADEHHPGTTSFGMSSFNLSNAIMGSGILGLSYAMA TG++LF+IMLL VAILSL
Sbjct: 61   KTLTDYADEHHPGTTSFGMSSFNLSNAIMGSGILGLSYAMANTGIVLFVIMLLTVAILSL 120

Query: 121   YSVHLLLKTAKEGGSLIYEKLGEKAFGWPGKIGAFVSITMQNIGAMSSYLFIIKYELPEV 180
             YSVHLLLKTAKEGGSLIYEKLGEKAFGWPGKIGAF+SITMQNIGAMSSYLFIIKYELPEV
Sbjct: 121   YSVHLLLKTAKEGGSLIYEKLGEKAFGWPGKIGAFISITMQNIGAMSSYLFIIKYELPEV 180

Query: 181   IRAFMGLEENTGEWYLNGNYLIIFVSVGIILPLSLLKNLGYLGYTSGFSLTCMVFFVSVV 240
             IR FMGLEENTGEWYLNGNYL++FVSVGIILPLSLLKNLGYLGYTSGFSLTCMVFFVSVV
Sbjct: 181   IRVFMGLEENTGEWYLNGNYLVLFVSVGIILPLSLLKNLGYLGYTSGFSLTCMVFFVSVV 240

Query: 241   IYKKFQIPCPLPVLDHSVGNLSFNNTLPMHVVMLPNNSESSDVNFMMDYTHRNPAGLDEN 300
             IYKKFQIPCPLPVLDH+ GNL+FNNTLPMHV+MLPNNSES+ +NFM+DYTHR+P GLDE
Sbjct: 241   IYKKFQIPCPLPVLDHNNGNLTFNNTLPMHVIMLPNNSESTGMNFMVDYTHRDPEGLDEK 300

Query: 301   QAKGSLHDSGVEYEAHSDDKCEPKYFVFNSRTAYAIPILVFAFVCHPEVLPIYSELKDRS 360
             A G LH SGVEYEAHS DKC+PKYFVFNSRTAYAIPIL FAFVCHPEVLPIYSELKDRS
Sbjct: 301   PAAGPLHGSGVEYEAHSGDKCQPKYFVFNSRTAYAIPILAFAFVCHPEVLPIYSELKDRS 360

Query: 361   RRKMQTVSNISITGMLVMYLLAALFGYLTFYGEVEDELLHAYSKVYTLDIPLLMVRLAVL 420
             RRKMQTVSNISITGMLVMYLLAALFGYL+FYGEVEDELLHAYSKVYT D LLMVRLAVL
Sbjct: 361   RRKMQTVSNISITGMLVMYLLAALFGYLSFYGEVEDELLHAYSKVYTFDTALLMVRLAVL 420

Query: 421   VAVTQTVPIVLFPIRTSVITLLFPKRPFSWIRHFLIAAVLIALNNVLVILVPTIKYIFGF 480
             VAVT TVPIVLFPIRTSVITLLFP+RPFSW++HF IAA++IALNNVLVILVPTIKYIFGF
Sbjct: 421   VAVTLTVPIVLFPIRTSVITLLFPRRPFSWVKHFGIAAIIIALNNVLVILVPTIKYIFGF 480

Query: 481   IGASSATMLIFILPAVFYLKLVKKETFRSPQKVGALIFLVVGIFFMIGSMALIIIDWIYD 540
             IGASSATMLIFILPA FYLKLVKKE RSPQK+GAL+FLV GI FM+GSMALIIIDWIY+
Sbjct: 481   IGASSATMLIFILPAAFYLKLVKKEPLRSPQKIGALVFLVTGIIFMMGSMALIIIDWIYN 540

Query: 541   PPNSKHH 547
             PPN HH
Sbjct: 541   PPNPDHH 547

>CRA|114000033649823 /altid=gi|10945621
          /def=gb|AAG24618.1|AF298897_1 (AF298897) amino acid
          transporter system A [Homo sapiens] /org=Homo sapiens
          /taxon=9606 /dataset=nraa /length=506
          Length = 506

  Score = 597 bits (1522), Expect = e-169
  Identities = 315/549 (57%), Positives = 383/549 (69%), Gaps = 46/549 (8%)

Query: 1   MDPMELRNVNIEPDDESSSGESAPD---SYIRIGNSEKAAMSSQFANEDTESQKFLTNGF 57
             M E+   +I PD++SSS S D SY   +++AA+ S +A+ D E+Q FL
Sbjct: 1   MKKAEMGRFSISPDEDSSSYSSNSDFNYSY----PTKQAALKSHYADVDPENQNFLLESN 56

BLAST Alignment to Top Hit:
>CRA|145000039337444 /altid=gi|12017941
          /def=gb|AAG45335.1|AF295535_1 (AF295535) amino acid
          transport system A3 [Rattus norvegicus] /org=Rattus
          norvegicus /taxon=10116 /dataset=nraa /length=547
          Length = 547

  Score = 975 bits (2492), Expect = 0.0
  Identities = 478/547 (87%), Positives = 508/547 (92%)

Query: 1   MDPMELRNVNIEPDDESSSGESAPDSYIRIGNSEKAAMSSQFANEDTESQKFLTNGFLGK 60
             MDP+ELR+VNIEP ++S S +S   Y +GNSEK AM SQFANED ESQKFLTNGFLGK
Sbjct: 1   MDPIELRSVNIEPYEDSCSVDSIQSCYTGMGNSEKGAMDSQFANEDAESQKFLTNGFLGK 60

Query: 61   KKLADYADEHHPGTTSFGMSSFNLSNAIMGSGILGLSYAMAYTGVILFIIMLLAVAILSL 120
             K L DYADEHHPGTTSFGMSSFNLSNAIMGSGILGLSYAMA TG++LF+IMLL VAILSL
Sbjct: 61   KTLTDYADEHHPGTTSFGMSSFNLSNAIMGSGILGLSYAMANTGIVLFVIMLLTVAILSL 120

Query: 121   YSVHLLLKTAKEGGSLIYEKLGEKAFGWPGKIGAFVSITMQNIGAMSSYLFIIKYELPEV 180
             YSVHLLLKTAKEGGSLIYEKLGEKAFGWPGKIGAF+SITMQNIGAMSSYLFIIKYELPEV
Sbjct: 121   YSVHLLLKTAKEGGSLIYEKLGEKAFGWPGKIGAFISITMQNIGAMSSYLFIIKYELPEV 180

Query: 181   IRAFMGLEENTGEWYLNGNYLIIFVSVGIILPLSLLKNLGYLGYTSGFSLTCMVFFVSVV 240
             IR FMGLEENTGEWYLNGNYL++FVSVGIILPLSLLKNLGYLGYTSGFSLTCMVFFVSVV
Sbjct: 181   IRVFMGLEENTGEWYLNGNYLVLFVSVGIILPLSLLKNLGYLGYTSGFSLTCMVFFVSVV 240

Query: 241   IYKKFQIPCPLPVLDHSVGNLSFNNTLPMHVVMLPNNSESSDVNFMMDYTHRNPAGLDEN 300
             IYKKFQIPCPLPVLDH+ GNL+FNNTLPMHV+MLPNNSES+ +NFM+DYTHR+P GLDE
Sbjct: 241   IYKKFQIPCPLPVLDHNNGNLTFNNTLPMHVIMLPNNSESTGMNFMVDYTHRDPEGLDEK 300

Query: 301   QAKGSLHDSGVEYEAHSDDKCEPKYFVFNSRTAYAIPILVFAFVCHPEVLPIYSELKDRS 360
             A G LH SGVEYEAHS DKC+PKYFVFNSRTAYAIPIL FAFVCHPEVLPIYSELKDRS
Sbjct: 301   PAAGPLHGSGVEYEAHSGDKCQPKYFVFNSRTAYAIPILAFAFVCHPEVLPIYSELKDRS 360

Query: 361   RRKMQTVSNISITGMLVMYLLAALFGYLTFYGEVEDELLHAYSKVYTLDIPLLMVRLAVL 420
             RRKMQTVSNISITGMLVMYLLAALFGYL+FYGEVEDELLHAYSKVYT D LLMVRLAVL
Sbjct: 361   RRKMQTVSNISITGMLVMYLLAALFGYLSFYGEVEDELLHAYSKVYTFDTALLMVRLAVL 420

Query: 421   VAVTQTVPIVLFPIRTSVITLLFPKRPFSWIRHFLIAAVLIALNNVLVILVPTIKYIFGF 480
             VAVT TVPIVLFPIRTSVITLLFP+RPFSW++HF IAA++IALNNVLVILVPTIKYIFGF
Sbjct: 421   VAVTLTVPIVLFPIRTSVITLLFPRRPFSWVKHFGIAAIIIALNNVLVILVPTIKYIFGF 480

Query: 481   IGASSATMLIFILPAVFYLKLVKKETFRSPQKVGALIFLVVGIFFMIGSMALIIIDWIYD 540
             IGASSATMLIFILPA FYLKLVKKE RSPQK+GAL+FLV GI FM+GSMALIIIDWIY+
Sbjct: 481   IGASSATMLIFILPAAFYLKLVKKEPLRSPQKIGALVFLVTGIIFMMGSMALIIIDWIYN 540

Query: 541   PPNSKHH 547
             PPN HH
Sbjct: 541   PPNPDHH 547

>CRA|114000033649823 /altid=gi|10945621
          /def=gb|AAG24618.1|AF298897_1 (AF298897) amino acid
          transporter system A [Homo sapiens] /org=Homo sapiens
          /taxon=9606 /dataset=nraa /length=506
          Length = 506

  Score = 597 bits (1522), Expect = e-169
  Identities = 315/549 (57%), Positives = 383/549 (69%), Gaps = 46/549 (8%)

Query: 1   MDPMELRNVNIEPDDESSSGESAPD---SYIRIGNSEKAAMSSQFANEDTESQKFLTNGF 57
             M E+   +I PD++SSS S D SY   +++AA+ S +A+ D E+Q FL
Sbjct: 1   MKKAEMGRFSISPDEDSSSYSSNSDFNYSY----PTKQAALKSHYADVDPENQNFLLESN 56

FIGURE 2, page 3 of 4

```
Query:  58 LGKKKLADYADEHHPGTTSFGMSSFNLSNAIMGSGILGLSYAMAYTGVILFIIMLLAVAI 117
            LGKKK   Y E HPGTTSFGMS FNLSNAI+GSGILGLSYAMA TG+ LFII+L  V+I
Sbjct:  57 LGKKK---YETEFHPGTTSFGMSVFNLSNAIVGSGILGLSYAMANTGIALFIILLTFVSI 113

Query: 118 LSLYSVHLLLKTAKEGGSLIYEKLGEKAFGWPGKIGAFVSITMQNIGAMSSYLFIIKYEL 177
            SLYSVHLLLKTA EGGSL+YE+LG KAFG GK+ A  SITMQNIGAMSSYLFI+KYEL
Sbjct: 114 FSLYSVHLLLKTANEGGSLLYEQLGYKAFGLVGKLAASGSITMQNIGAMSSYLFIVKYEL 173

Query: 178 PEVIRAFMGLEENTGEWYLNGNYLIIFVSVGIILPLSLLKNLGYLGYTSGFSLTCMVFFV 237
            P VI+A   +E+ TG WYLNGNYL++ VS+ +ILPLSL +NLGYLGYTSG SL CMVFF+
Sbjct: 174 PLVIQALTNIEDKTGLWYLNGNYLVLLVSLVVILPLSLFRNLGYLGYTSGLSLLCMVFFL 233

Query: 238 SVVIYKKFQIPCPLPVLDHSVGNLSFNNTLPMHVVMLPNNSESSDVNFMMDYTHRNPAGL 297
            VVI KKFQ+PCP+     + N + N TL     ++P
Sbjct: 234 IVVICKKFQVPCPVEAA--LIINETINTTLTQPTALVP-----------------------269

Query: 298 DENQAKGSLHDSGVEYEAHSDDKCEPKYFVFNSRTAYAIPILVFAFVCHPEVLPIYSELK 357
            + +    +D C P YF+FNS+T YA+PIL+F+FVCHP VLPIY ELK
Sbjct: 270 ------------ALSHNVTENDSCRPHYFIFNSQTVYAVPILIFSFVCHPAVLPIYEELK 317

Query: 358 DRSRRKMQTVSNISITGMLVMYLLAALFGYLTFYGEVEDELLHAYSKVYTLDIPLLMVRL 417
            DRSRR+M  VS IS   M +MYLLAALFGYLTFY  VE ELLH YS +   DI LL+VRL
Sbjct: 318 DRSRRRMMNVSKISFFAMFLMYLLAALFGYLTFYEHVESELLHTYSSILGTDILLLIVRL 377

Query: 418 AVLVAVTQTVPIVLFPIRTSVITLLFPKRPFSWIRHFLIAAVLIALNNVLVILVPTIKYI 477
            AVL+AVT TVP+V+FPIR+SV  LL   + FSW RH LI   ++A N+LVI VPTI+ I
Sbjct: 378 AVLMAVTLTVPVVIFPIRSSVTHLLCASKDFSWWRHSLITVSILAFTNLLVIFVPTIRDI 437

Query: 478 FGFIGASSATMLIFILPAVFYLKLVKKETFRSPQKVGALIFLVVGIFFMIGSMALIIIDW 537
            FGFIGAS+A+MLIFILP+ FY+KLVKKE +S QK+GAL FL+ G+ M GSMALI++DW
Sbjct: 438 FGFIGASAASMLIFILPSAFYIKLVKKEPMKSVQKIGALFFLLSGVLVMTGSMALIVLDW 497

Query: 538 IYDPPNSKH 546
            +++ P  H
Sbjct: 498 VHNAPGGGH 506
```

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF01490	Transmembrane amino acid transporter protein	187.0	2.9e-52	2
CE00398	E00398 CD53	4.0	4.8	1

Parsed for domains:

Model	Domain	seq-f	seq-t		hmm-f	hmm-t		score	E-value
CE00398	1/1	90	110	..	1	23	[.	4.0	4.8
PF01490	1/2	99	236	..	1	179	[.	58.9	2.5e-14
PF01490	2/2	305	529	..	200	467	.]	133.9	3e-36

```
   1 AGCTTAGCAA TATGGATCAA GAGGTCCAAT ACCTGATTAA TAAAAGTTTC
  51 AGGAGTAAAC AAAGGGGAAG AAATAGTTTT TTTAAATAGT AGAACTTTTT
 101 TTATTTTTAG AAAATGTGTC TTCTATAGAA GAAAGACAAG CCTTTTGATT
 151 GGGCCGTCTG CATGCTGAGT ATGATGAATT TTAAAAGCGA CTCACATCTA
 201 GTCACGTCGT GATGAAAGGA TAAGGATAAA AATTCTGAAA TCCTCAGAAA
 251 ACCATCGATA AATTATCTAT AAAGAAATAA GAGCCAGACT CATCAATAGA
 301 AGCTAGAAGA GAGAAGTTTC TTCAATATTC TGAAGGAAAA TGCTTCTGAA
 351 TCTAGAATTC AAACAATTAA CAAAGTTTGA AGGCAAAATA AAGAATTTTC
 401 CAACATGAAG CAACTCAGAA ATTCTATTTA CAGACATAGG CTCATTGTGT
 451 GAAAAAAGTT ATTCAAGGCA TTATTTTAGC ATAATGCAAA ATAAACTGAA
 501 GAAAGAAGAT AGAATGCCGT TCAAGAAACT AGCAGCTGAG CAAGACTCAG
 551 AGGTTGGAGG AGGAAGCCAT TCAGAATGAG AAAGAGCATA GAAAATTTGC
 601 TTTCAAAGTT TTGGTAATAT AGAATTATAT TTCACTTATT ATGTAGTCAA
 651 ATACACCACT TTGTCTTTAG GGCATACTAT TTATACAGTG ATAATACTGT
 701 AATTGCTGCT TATTGGTTTT CCATGTTTAG AAACAACCTA CAGGCAAGTT
 751 ATGACACTTG TTTCACAGAA CAAGATGAAA ATATTATGAT TCTCAAATTG
 801 TAAAAGTATT TTATTAACTA AAATAATTAG GAGTGTAGGA GAAGGAAGGA
 851 AAGAAAGAAA AAGTATGCTA ATGTCCTTAT TTTTTATGGG TAACCAGTCT
 901 AAAATCAGTA AACCAAGTCA AAAAAGCTTT AGTGAATTAT TCAGATCTAG
 951 AATGGCTAAC TTTAAGTAAC AAGCTAAAAA CAGAAACCGT CAATAGTGGT
1001 TGCTGCTGGG AAGTGAGACT GGTACTGTGT GAAGAATGAG GAAAACCTTT
1051 GTACTCATTT AGTGAGTTTC TTTTTTTTTT CTTTTACCCA TATGCATGTC
1101 TTACTTCTAT TCTCTCTTAG CTTTTAACCT GCTTCTTTTC ATCTTTTATG
1151 TATATACATT TAGGCTGCCT TATATTAATA ATAGTTTCAT TTTTGTTCCT
1201 CCTGCTTAAA ACACTGTGTG CTATTTTTTT AAATTCTGAG AACTGCTTTC
1251 TTTATTTCTA GACAATTCTC TGCCATTATC TCTTTCTGTT TTGTCTCACC
1301 CTAGTCTCAC AATTCTCTAT ATTGGAATGA CTATCAGTGT ATATTTGAAC
1351 TTGTAATTCT TATTTTTTCC CCATTCCTCT TAACTTCTTA TTTGTATTTT
1401 TCTTTTTTTA ATCTCTTCAT GCTATAATTT GAGTGATTTC CACAGATCTG
1451 TCTTTCAATT TTATAAGTCT TCCTTCAGCT GAGTTTTTTT AAATTTCAAT
1501 GATTCTATTT TTTTCTTTTT TTTAAGAATT CCTTTTTTTG ACTCTTTTTG
1551 CAACAGCCTG TTCTCCTTTT ATATTCCTTT ATAATGTTTT TATTCTGTGA
1601 AAGTTATTCT CTTATTTTGA ATGTTTTCTT TCAAAATGTC TTTCTTTTTA
1651 TTAATTTAAT GTAAAAGTCC CTTTTAAATT GCTTTGTTAT TTGTAGTTCC
1701 TTAGATGTGA ATTTTATCAT TTCTTGTGCC TACTGGCACT CTTGCTAGTG
1751 AGTTTCCATG TGTGTTCTAT ATGTTTTGTA ATTTGAGGAT GTGAACTTTT
1801 CTCAAGTGTG AGTTGCCTTT CAAAAAAGTA CTGCCATGGC ACTGGGTTGT
1851 GGAGGTATTC CCATGTGGTA GTTTCTGTTT GTCAGAGGAA TAGCACATTT
1901 TGTGACTTCT GGAGCAATTT TTATGTTAGT TTCTCTGCTC AAGATTTCCT
1951 TATCAAATGG GTATTGCACA TGTCATGACC ACACTTTTCA AGAATGATAG
2001 TGTTTCTCCT AATACGATGG TTCAACAATA ATTGAATGAA TCTAATGGTA
2051 AGAATTTCAG AAGAAATTAT ATCAACTACA TATAGTAGAT TCAAGGCATT
2101 TTTCAAAAAC ACAATGCCAG TCCACCCCTT TTCACTATAC AATTGAGGAA
2151 AATGAGGTCC CCAAATGTTA AATGACTTCT GCTGAGATCC AATGAATTAA
2201 AGGCAGAGCA GAGGCTAAAA TCTAGATCTC TTTGTTGTTA AAATACATTT
2251 TAATTTGACA CAGATGATGA GTAATGCTGA CCCAGAGGTA AATCTGAACT
2301 TTCTTTTGTT ACTATTCTTA ACTTTGGCTT CAGGATCCAA GTGCCTAGAA
2351 AGTTACTTCC TAAACTTGAT CCTCACCTAT GTTGCATATT ATCAAGCATT
2401 TGGTGGTGTT AATTCTTTCA TGTCCAATTA AATTAAAGCA GTAATTTTCT
2451 TTCTAGTTAT TGCTAGTAGA GACACTGGTA GATTCTGCCT TGGTAGACCT
2501 TCCTCTGTCA ACAATTTACT TTTGTCTTCC TTTCTTTTAA AACATGTATC
2551 CCACTCACAA ATACCTAAAT TTCCTTGAAG ACTGCTGCCA TGTTTTAAGA
2601 TTTCTTTTTT TTTCCATAGT GACTAGTAAA ACCTGCCATT TTCATTATAC
2651 ATAGGCACTC TATAAATATC TGCTAATTTA GCAATTATTA GTAATTTCCT
2701 TTCTTCTCTT CCATTTCTTC CTTTCTTGTA TTGGGTAAAG GAACATTTCA
2751 GGATTTGCTT ATGTAAAGTT TTCAGGAGTT TCTTTCCTTC CTCCCTTTTA
2801 CAGAGAGCAT ACAAAATGTA GATGATTCAT ATTCACTTAT TTCATTTAAA
2851 TAAAATTATA ATGATGTATG TTGTGTTCTG TTTGCAGAAC AGAGTGTTCT
2901 GAACATCAAC ACAAAGTGGA AGAACCTTAA GCTGAAGGTA CAGTATATTA
2951 TTTACACTGA AGGGGCTTGT GTGTGGACAA GAAAGCGCTG ACAGCTCAAA
3001 TGGATCCCAT GGAACTGAGA AATGTCAACA TCGAACCAGA TGATGAGAGC
3051 AGCAGTGGAG AAAGTGCTCC AGATAGCTAC ATCGGGATAG GAAATTCAGA
3101 AAAGGCAGCA ATGAGCAGGT ATGGGGTTAA AAATTACTAT GTTCCATGGA
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3151 AAAATAAGAC AGGATGTGGA CATGGAAAAC AGGGTCTTGA TGGGAAGAAC
3201 TGGATTTATT ACAGGTAAAT TTGTGATAAC AATGATATTG ATGCTAGCAC
3251 ATCAATTCCC TGGTCCTGAA ATACAGTGAT AATGTCAATC TCTTTTGTGA
3301 CTGATTTAGA ATTGAGGTTA CAATGTCTTT GTCTCCATTA ATAATGTGTA
3351 ATAATTTTAA TTATTTTAGC CTATTGCTCC TCTTATCTTT CTCAGATTCC
3401 TCTTTGAATG TTGCTACACC TCCTGGTTTC TGTAGGGATT CTTTTCTCTC
3451 TAAAAGTATC CTCTGGGCAA GCTCACTCAC AACTACTATG GCCTCACCCT
3501 CCAAATATAT GCCATATACC CAGCCTGTTA AGTTTCTCTA CTGAATTTCA
3551 GATAATTATA TCTGAATGTC TACTGCACGT CTCTACTGGA CCATTACTGT
3601 GTCTAAATTG CCTCATTTAT AAAGTTAAAC CTGTAATGTC TAATACTGAA
3651 CTCCTATCTT TCCCTCCAAA ACCTGCTCCT CCTCTAGTAA TCCCCATCCT
3701 AGTGAAAATC ACTGCTATCA TGTAGCAACT CACTCAAAAG CCCCTAGGTG
3751 TAAACTTTGA CCCACATAGC CAACGGTCAG TCATATCCAG TTGGTTTGAC
3801 CTTATTAATG CTTCAAATAC ACCTACTTTT CTGTACCCAT TCTACTGTGG
3851 TCTTACGTTA GGCCTACATT AAATGTGAGA CAGGGAGAGA GCCCTGATTT
3901 CTCTCCCTGT CTTACATTTT GCTCTCCTCT GTCTAGCCCT CTACACTCCT
3951 GCAAGAGCAA TCTCTTACAA TTGCAAATTG AATCAATTTC CATCCTTAGA
4001 TAAAGCCCTT CTGCACCTCT CCAATAGCCA TAAGAGAAAG TAGATTACAC
4051 ACACTGCTGG GCACGTAAGG TCCTTTGTGA TCTGTTCTTG ACCTGCCCCT
4101 CCTGTCCTGT TTTTTGCCCT CTCCCTATTT GTTACTTGTT GCCTTCACTC
4151 ATTCTGCTCC AACTGCCTGG AATCAGTCAC CTGCTCCCCC TTTCTCCGTG
4201 TTGACACCTC TCATCCTTCA AGAATCAGCT CAACATCAGG TCTCCTATGC
4251 AGCCTTTTCC AAATTACTCT ACTCCCCCAT GTAGAAGTGA CTGCCCCTCC
4301 TTCATGTACC CTCTCCCTGT GCAGATGTTA ATTACGCCAC TACTACAGGT
4351 TAATGGCCTC TGTGGTCCCA CCACCTGCCA CATTGTCTGG TGCATAGTGA
4401 GTGCACAATA GTTATTTGAT AAGTCAATTG ATTTCCCACA AAATGTTATA
4451 TCAAATTGTA CATGATTTAA GATGCTCAGA AGGGAATTTT TGACCAAATC
4501 TAGGCGTGAA ATAGAGAATA TTGTGCTCAA ACAAAGACTT CTCATTTTAT
4551 TTACAACACC CAGGAAAATC CATCAGGAGA AACTACCGTT CTTCCTTCAA
4601 GTAGCTCAGT GCAATGAACT TTAGGGATGT CGGACTAGAG AGGCCACTGA
4651 GATGTAAATT ATAGCATTTT CTAAATTAGG TGACCCTTGA AGAAACACTA
4701 GGGTGCTAGA AGACAGGGCT TTGGAGTCTG CAGAGTAGTT GCCTGACTTT
4751 AGAGAAGCTG TTTGTCCTCT TTGAGCTTCA ATGGAAAATG TAAAATGGCA
4801 AACCAACAGC TGCTTTTCAA GGATGAGATG GGTGACCAGA ATATAGATGA
4851 CATTCAATAC TTTTTTATTA CTTCTCCTTC ACTGCATTAC CCTCAGTAAA
4901 TTGATTCAAA CCTGAGGATG TTTCTGAAAG GCATGCACAC AAATATGAGC
4951 TCTGCCGAGG TTGACAGAGT TAAAGGGGAC ACCCTCCTAA GAACTGTCAT
5001 AGTGTCATTC CACTTGATCC TCAAAAGCCA GAGTAGAAAG AGCATGAATG
5051 CTTTTCTTAA GCTTCATGCA ATGTGTTCCG AACCACTCAC AGTGACTTAC
5101 CTTTTATCTC CTGGCTTAAA CATAGGACAT CATTTTGCAG TTTTTAAAAT
5151 CAGTTTAAAG AGATGGGTTT TATCTATGTG TGGTTTGGAT TGAACCCTTA
5201 AATGTAAATT TTTGAGAAAT TCAACATAAT GTATTTATTT GTGATCATTA
5251 TACTTGTGTT TTCAATACAT GCTGGGTTTG GTATCAAAAC ATTTAACATA
5301 CTGGGGACAT TTCTCATCTA TTTTATACAA TCTTGGCATG TTAAATGACT
5351 ACAACTCATC TCATGCCAAA ATAAGAACAT GCAAATGCCT CAAAGAAAGA
5401 AAATCTGTTT ACTTTCAAAT TCTCAATTTT AAAAACTACT ATGGAATACA
5451 GATTTTAGTT TATTGATTAA AATAAAGATT CCAGAGTTTA AATTCTAGGT
5501 GGCACTTTTG TTTTTATAGT CCTCAGGCCC ATTTTAGGCT TCATTTTATC
5551 CTGTCATCTC AGTCTCCAAC TGTGAACATT ATGTACCAGT CTTCACATAG
5601 CAGGTACATT AATTACAGAC CATTAATGTA AACCACAAAA GAGTGGTGGG
5651 CAGTGGGTGG GGGGTGAATG GAAATGGAAA GAGGCAACAA CTGAGGGCAT
5701 TGTGCTTTCT GTGAGAAATA TGGGGAGAAG GCTAGGAAAT GTTCTTAACT
5751 TGTGTACTCA GAGCTATTTA TGCCTTGAGT TCTAGAAAAG CACATACAAC
5801 TTTGTGGTTT CGTGTGCTGT TTCTATCTAC ATCTCATACT GTTTTCTATT
5851 CTCAAAAAGT AACCCTGTCA TCCTCTTTCC TCTCCAGATT ATTTTCAGGA
5901 TTAGCTTCTG TTATAAAAAA TAGCTTGTAC AGATCTCCTA CAATAATTAT
5951 TTTCTATTTT ATTTCTAAGG TTTATTTATT TATTTATTGA GACAGACAGA
6001 GTTTCACTCT TGTGGCCCAT GCTGGAGTGC AATGGTGCAA TCTCGGCTCA
6051 CTGCAACCTC TGCCTCCCAG GTTCAAGCGA TTCTCCTGCT TCAGCCTCCT
6101 GAGTAGCTGG GATTACAGGC GCCTGCCACC ACACTCGGCT AACTTTTTGT
6151 ATTTCTAGTA GAGACGAAGT TTCACCATGT GGCCAGGCT GGTCTTGAAC
6201 TCCTGACCTC AAGTTATCCA CCCACCTCAG CCTCCCAAAG TGCTGGGATT
6251 ACAGGCGTGA GCCACTGTGC CTGGCCTCTA GGATTATATT AATAGAACAA
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<div style="text-align: center">

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6301 TCTTCAATTA TTTTATCTTT CTTTATCTTT CTTTTCATGT AGGAAATGTC
6351 CTAAAATTTT CAAACCCTCA ATTTGAAAGC ACTTTTAAAA TCATACATAG
6401 TCGAGCATTT TATATAAAAA CAACTAAAAA GTCTGTGACA TTTTGCAGTA
6451 TAAAAATGCA ATGGCAGCAG CAGGCCTTAT TAATTGAGCC TCTTGGAAAT
6501 GTGGCTGGTC CTAGGTCCGT AGCCTCAAAG GCCCTGGCTT GTAACTGCAG
6551 GAGCTGACCA GCACAGCTCT ATAACCAAGT TGTACATCTT CTAGCCTGTG
6601 TCCAAGAAAA CCAGAATCAC AACGCTCTGT GGATAGTGAC ATCTTAAAGT
6651 TTTCTTTCCC TCCCAACTCT TTTGCCAGTT CATTGAATTG CTTTAATAAT
6701 TTCCTTAGTT TCATTCATTA TCTGTTAATA ATCCATGTAC ATTTTGAGAG
6751 TAATTAAAAC ACATACGCAC ACACAGAAAC AACCAACACA ACACACAGCT
6801 ACCACTGAAT TACTTTCCAG TAAGAGATGT ATGTATAAAT GATTGTACCA
6851 AAAAAAAAAA AAGAAGAAA ATACCAGCTA CAGGGCCCTG CCTGGGACTG
6901 CTTGATGCCA GGGGGAGAAT GGGGTCTCCC CCTGGGTATG GGTGGGTATG
6951 GGCCTGCTGC TTCACCTTTC TGAGCCACAG TTCCCTATAG GGATATTTTG
7001 AACATCAGAT GAGATAAGGA TCACAGTGCC TAGGCATTTA ATAAATATTC
7051 GTTGAATTAA TAAAATCATC TGATTATGGT ATGGTAGTAG TTCAGAAAAT
7101 TCTGTCATAA CCCTGTACTC TTTCTTTGGA AGGGCTCTAA ATGGGAACAC
7151 AATTAGTTGT AGTCTCTTGC ATAGCTAATG TGAGAAAGAG GGAATGTGGT
7201 ATAAACAATT TTTTAACTAA AAATAATATT TCCTTCCTTT ATAACATCCT
7251 TCTTCCATCC CAAAGTATAG TTGTAAATGG AACTCAAAAT TGTTGGTCTG
7301 GAATGACCGT TAGTGTGAAG GAGGAAAAGA AAATTGGGGT GTCTTATTTC
7351 CCCTCCTCTG ATTCAGTTAC TTAGATCACC TGAAACATAC ATATGATTCA
7401 GAGCATATAT TTAGATGTTT TCACTTTCTT ATTTGTGTGT GTGTGTGTTC
7451 AGTCAATTTG CTAATGAAGA CACTGAAAGT CAGAAATTCC TGACAAATGG
7501 ATTTTTGGGG AAAAAGAAGC TGGCAGATTA TGCTGATGAA CACGTAAGTG
7551 AATCTATGCT TTCAGGCAAT AAACGGGACT GAGGGTGTCT GATCTACCTA
7601 GGTCTCTGTG GGAAAACAAT GTGACTGAAA TTTTCCAAGC CTTGATCAGC
7651 ACATTCTGTG TTTATTCAGG CTCTTACTGG AATAAGGGCT TGTTTTTTCC
7701 TGTTCGCCAT ATGGCTGCAT GAATCATTTA TGAAACTTAT GTGTTTTGGG
7751 GGGAAATCAT TCTAACCCAA AGGTAATCTA CAATCATACA TGTTTTCCCT
7801 TCTTTATGTG ACTCCCCTTG TAATTTGTAT TTTTACTGAG GCCTCTGCTG
7851 AAACCAAGCA CTGCATTCCG TTGAAAATTA CATGCTTTTA TTGATGTTGA
7901 GTAATGGCTT TACTCCTGTA ATGTTATCTT AGTCTTCAAT TTTGGACTGT
7951 AATCTGCAGA TAATGTGAGA ATAAGGATAA CCCCTAAAGG TATGCCCTTT
8001 GGCAAATGTT TGCTTATAAT ACATCCCTTC TTTTTCAAGC ATCCCGGAAC
8051 CACTTCCTTT GGAATGTCTT CATTTAACCT GAGTAATGCC ATCATGGGCA
8101 GTGGGATCCT GGGCTTGTCC TATGCCATGG CCAACACAGG GATCATACTT
8151 TTTATGTAAG TGAATGTATA TGTCTACATT TGGTGATGAA GTCCATGCAT
8201 ACCTGGTGGC TTTTTCAATT AACAATCTCA AGTTTGATCT TTGTGAACGT
8251 GAAGACTCAG AGGAGGCTAA TCATGGCACT TGGTCACCCA ACCATCCCTA
8301 ACCCAACGGC AGAAAGTGTA TGTGCTCAAT CAACCAAAGT GCTGGAGCAG
8351 CCTCGCCAGA AGAATTTTGT TATTCAGTAA ATACTTGAAA TAATTTGGTG
8401 TTTAGCAACC AAAAAGATCT TTCCCAGAAG CAAATCTGAT TTTATCTCAT
8451 TCTTAGGAAA GAAGCAACCA AGCCTAAGAG CCCTGCATGC CCTTGCCTAC
8501 CTTATGTCCC ATTCCCTGTA CCCCTGTGCG ACAGATACAC TGGGCACAAT
8551 AGCCTTCTCT CCATCCTATG AAGATGCCAC ATTCCCTCTC ACCATTGGAC
8601 CTTTGCACAT GGTCTTGGAA CCCTCTTCTC TTCCTTCTTC ATCTAGTTAA
8651 CTCCTCATAT GTCAGTTCAG TCTCACCTGA ATACTGCGCG CCCTGATCTC
8701 CATGACTGGG GCAAATCACC TTATCATAAC ACTCACCACA ATTTTAATGT
8751 TTTAGTGCCA TTTGTCTGAT TCATTTGGTT AATATCTGTC CCTCTTGCTG
8801 GACTATAAGC TCTAGAAAGT TGAGCCCATG TCTGTTTTTA CTCACCAATG
8851 TCTCTACCTC CAAACCTAGA GCAGTGCCTG GTACAGGCAA TATTTGTTGA
8901 GTGACCAAAC CTTATTCCTA AACCTACGTA CTTTCACCAA ACTTGTTCAA
8951 ATGCTGCCTA AGGGTAGCAG CATCTGGTAG TTGACCTGTA GGGTGGATAC
9001 TGCACTGTCT ATGACAGACA ACAACGACG TTTATGTGCA TCATGTACAG
9051 CCTGGCATTT TCCAGGATAT AGTTGGCAGC AGTGGAATTC TTCACAAGAA
9101 TAAAGTCTGA TGTTAGGCAC CACTGTGGAC ACAGATCCTA ATCCCAAATG
9151 CAACGCTAGA GAGTTAAATA ACTGTCTAAG AATGCAACAT TTATATCACA
9201 AATATGTGCT GTTTATGTTC TGAATATCAC ATATGATTAG TAATCACACA
9251 GCTATTTGAG GGCTAAGCAT CAGGACTATA AATATTTGTA TTGTGTTAGT
9301 GCTTTGATTG AACTCTTTTA TGTATAATAT TCTTCAGCTG AATGGGTTTT
9351 TATATCAACT TTACTTTTAT ATAAGCCATG TTTTGAAATA AACTAGGATT
9401 TTAATAATCT GAATTTTAAT AGCTATGTAT GTAGTCATAT ATTTGTATGC
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 9451 TTTTGTAATG TGCTTACCTC TAAGACAAAA AAACCTGCCT TTCCTTATTA
 9501 ATTATACATA CCATTAAAAT GAATTAGGAA GTTACAGATC ACTGATGAAT
 9551 AGAAATAGGA AAAACTTCCC CCAATCCCAC AGTCATAGAT CATCTTCATG
 9601 AGAGAAGAAT GTTCCACTTT TTAAAATGAG GGCCTCATTT TAGGCTTATA
 9651 AACACTTAGC AGATGAATTT GGTCAGAACA ATTAAATCAC TAAACATCAT
 9701 GGGGTGTGTT TTGTGTGTCT AAGTAGCCCA GACTGGATTA AGCTTTCTCT
 9751 CTTAATTTAT AGCAAGTGAC ACAGTATTTT AAAGGTTTTA CTCTTAGTAT
 9801 TTTCTGCCAG AGAAAGTACA TGTTTAGAAT ACAGGGAATG CTCATTATTT
 9851 TTCCAGGGAA CAAAATTATA TAATCTGAAT TACATTATTC CTTAAAAACA
 9901 GTTAAGTTCA TAAGGCATAT GGAAAAATAT AGGAATAAGT CATTGGTTAG
 9951 ACAGTTCTGG CAAACATACT CTATGGAAAA TAAGAGTGCA ACATAGCTAC
10001 AGGGGTTATA AAATTTATAA TTCATGGTCC AAATGTACAT TTGTAGTATT
10051 GATTTCATTG GGAATTACCA AGGGATTAGA TCAATTGTGG GGAAAGTGTA
10101 TTTTTTAAAA ATAAACAAAG ATAAAGATTT TTTTTCTGAA TTCCAGGTAA
10151 AAGGCAGCAT TGCTCCTCCA TTTATTACGT AGATGCTTCT ATCAACATTC
10201 TTATTTTTGT GCTCCAAATC TTGGATTTGG AAAAATACCA ATCCGTATAA
10251 ACATAAAGAA ACCATACATG CATGTGGGGA TCCTAACACC AGAAATGACT
10301 CTGAATGCAA AAAAAAAAA AAAAAAAAA GGGAATTTTC GTGCCCCATC
10351 CTTAGCTTTC TCTGCTTTCT CTATTATATA TGCAACTGCC TGCCCCTCTA
10401 TCTTACAAAG TACTTCGTAA TCTAATGCAC AGGATCAGCA GTAATGCAGC
10451 TCAGACTGCA TGCTTTCGCC TTTGGATTCC TAGATTTCAG ATTAAGGTTT
10501 AGTCAGGCTA TTGAATAGCC CTTCAATTCT AAGTGCTGAT GTGAATATCA
10551 TGCAAATATG ATGTACATAT TCCCATGTGC TGAGTAAGTA GATGTAGCAT
10601 TTGCTAATGT TGCTATACAT TTAGCATCTA AGTTATGAAC CAGATTCTAC
10651 CACTGGGTAA CATTAAAAAA AAGTTAGGGA CTTCAGGTAT GTAAAATATA
10701 GCAAATTCTA TTTCTACGAC TTTAAAGGGT ATGTGTAGAG TTCTGAAAAG
10751 AATTTCTCAG CCTCCCCCAA ATCCACATAC TTTTGGAAAG CTGATGATTG
10801 AAAAGATTAA TGTGATCCTT TATTGTAACA TCTAACATAA TTACATTTTA
10851 TTTATTGTAG AAACTTTATT ACCTACTCTC TCTTCCCTTT GCAGAATCAT
10901 GCTGCTTGCT GTGGCAATAT TATCACTGTA TTCAGTTCAC CTTTTATTAA
10951 AAACAGCCAA GGAAGGAGGT ATGCTACCAC TTGAGTCCAA CACATTCTAT
11001 TTTAATTCTC ATAAAAGAGT ATTTCAGTCT GTTGCTTCAT AACCTTAGGA
11051 TGATTATAGT CAGTTTCACA TTTCATTTTC TTCTGAGCCC AGTGACACGA
11101 TCTCTCAGTG TTTATAGTTG TTTGGGCAAG TGAGAGGCAG GAGTGAAAGT
11151 CAACTGGCTC AGGTTCAAGA CAAATAGAAA AAAGAAATTT CTGATATATG
11201 ATAGAAATAA CTGTTTTGAC TTGCTACATG CAGCTAAAAT AAATAAAACC
11251 ATTGATTCTT GTTTGGAGAA CATTTTGATA TATTGCTTAT TGGTTTTTGA
11301 GGTTGCATCT TTTGGGCTTA TAATTTCTAT ATGATGTTTA TTTACATGTT
11351 TGAGACTCCA GCATGGAATT ATATGACAAA AATATTTTAG TCATTAAAAC
11401 AATCTCTTTA ACAAGGCTAT TTTATCTTTG ATTGTAGGGT CTTTGATTTA
11451 TGAAAAATTA GGAGAAAAGG CATTTGGATG GCCGGGAAAA ATTGGAGCTT
11501 TTGTTTCCAT TACAATGCAG AACATTGGAG GTAAGGGGAT ATACTTTCCA
11551 ATGGATCCCA TAAACTTTCT ATAGCGTGTT CAATAAATAA GAAAACTTAT
11601 GGCAATAAAC AGGCACTTTA GATACAGAAA AATTGCTACT TATAGTTCTT
11651 AAATTTTAAA ATGATAGTTT CTTAAATAGG TTTGTGTCCT GCTTTAATTA
11701 AAAACAGCAA TATCTAAGAA TGAAATAACA TATAAAACCC TGCCAATTGA
11751 ATTCTAGAAT TAAAATATAA AATAAAAGCT TTCTTGATTT TTAATGTTAT
11801 TATAGCATGA ATTATTACTC TTAAAAATTG AAGAATTTGT GCTTATATCT
11851 GTCATTGACA AAACAGTTGA CGTTTTCTAT GTGTGACTGA GTTCGATTTA
11901 CTAAACTGAA AAGTGGGTGT CTGGGGGAAC ATAGCCAAAT GCTGTGGTCC
11951 TTGAAACGCA GCCTGCACTG AGCCAGCCCA CTAGACAGTG TCTCTGGAAG
12001 TTTACTAAGG CAAAAGTCTG GCTAGGCATC AAATGCACTA TAAACCCCGG
12051 TTTGTTGATT CTATGGATTC TTATAATTCC CACTGAATTA TCATTTCCAG
12101 TGTAGGACCT AGAAATATAT ATATATATTT TTAACAATGT TCTCTCGTTG
12151 GTGTGTTTGC CCACCAGCTT CATACTGTTT CTGTTGTGTC TTTGGCCCTC
12201 AGAAGGCATC CAAACCCATA TTTCAGATGT CCTGCCGGCT GCTTCCTGGC
12251 ACATGGCCCC AGCCATCTCC CCACATAATG ACACTTACTC CCTCACCTCC
12301 TACCCAGTCC CTAAACCTGC TATTCTATTT CTCTGATCTT TCTTTTCTCA
12351 GTGAATACCA CCAGCAGTCA TCCAGTTTCT GAGGGCAGAA ATCTGGATGT
12401 CAGCGTAAAT GTTTCCTTTT CCCCAACTCT GCATGTCCAA TCAAATGGCA
12451 AAGTCTGTTC ATTTGATCTC TTACTTATCT CTTGAACCTC TCCTCTCTGT
12501 CCGTCCTCAT GACCACAGAT GATCACCATT TATAGCTCAG ACTATTGCAG
12551 TAGTCTTCTA ACTGGTCTTC CTGGCTTGAG TTTCCCCTGC TCTCAGATAA
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12601 ACTCTAATTT GTTCTCCAGA TAAACTTTCT CAAATTTGAG TCTGTTTCTA
12651 CTTTTGTCGT GCATAAAATT CTTCAGCATG CCTTTATTAT TTTCAAGGAA
12701 AAACTTAAAC TCATTGGACT GACACAAGAT CTTCGTCTAG TTCTTCTGCT
12751 CAATCTTTCT AAACTTTCCT AGCAATGCCC ATATCTATCT ATCTTTATCT
12801 ATCTATCTAT CTATCTATCT ATCTATCTAT CTATCTATCT ATCATCTATC
12851 AATTTATCCA TCATCTATAC CCTACATGTC CTGTGTCAAA CCATAACAAA
12901 TTATATTTAT TCCCCTAACA GTACTATTTT AATATTTTTA AAAATCATCC
12951 ATGCCTTCTT TTCACAGGCT ACTTTCTCCC CTTGACTGTC TCTCAAAGTC
13001 CTCCAACCCT AACACACACG CACACACACA CACACACACA CACACACACA
13051 CACACACATT TTCTCTCTCA CTCTGCTCAC CTGGTCTATT GCTCCTCTAG
13101 ACTGGTAAAT ACTAGTTCCT CTGGGCTCTC ATGGTCCTGT TTGTATCTAG
13151 TATGTTACTG TTTTCTAAAG GATATTTTAA AACACTTGAG TAGAGAATAA
13201 GCTTTTGGAG TCTGATGGAC CTGAATTTGA GTCTGTTTCT GTCACTATCT
13251 GTGAACTTGG GAAGATCACT GTACTCCTTT GTCTGATTTT TTCATGTATA
13301 AAAATTACCT TACAAAGGCT ATTGTGAGGA TGAAATAAGG TAACATATGG
13351 CACATAATAA GTGTTCTGTA TATGCTTCTC TCCTCCCTGG TTCTCTGCTT
13401 CCATATCCAT GTCTCTGGAG TTGCCTGAAT TATTTTTTAA ATAGGCATTT
13451 AAAAAATTAT AAAACAAATA TATGATGATT GTGAAAAACT AAAACACTGC
13501 ATAAATATAT AAATTACCAA GAAAAGTTTA TGTCAGTCAT CCTCAGAAAT
13551 AACTACTCAT AGGTTTTCCC CTATGCCTAA TTCAACAAAT ACATTGAATA
13601 TTGTTAGTAT TGGATCATCT TATGATACCG ATTTTCAGCT TTCTTTTTAA
13651 ATTTAACAAT ATGCCTTGAA TATATTTGCA TGTTATTCTT TTTAATGATT
13701 TTTGAGGTTT CCATTACACA AATGTGCCAT AATTTGTTTA CAGTATCCTT
13751 ATTGATGAAC AGTTGGATTG TTTCTAATTT TTCACTGTTA TAAAAATGCT
13801 ACAGTAAATA CACTTGCACA GAGATCTTGC AAACAGGCAA CCCATTTTAA
13851 TAAATAAATT CACTGGAGTT ATCAAGGATT TCTGGAATGC AGAAATTTCT
13901 TTAGTAATCT ATCTAACTAT ACTCACCCTG ATAATGGATA GTTGGTAAGC
13951 AGATAAGTAA AATTCAGCCA TATCTTATGA TTTGTGTTAA AAAAATTTTT
14001 ATATGTTAAG ACTACAATCT TGGGTAGAAT TTGACAGTAA TATCAAAATT
14051 GTCTCATTCA TTTTACTGGT TTGGAGCCAT ATGCATATTA GCCCCCCAAA
14101 TCCCAACAAA TAGACCACTT TACATTTGTT TCAAACTCTC AGCCTTATCA
14151 AGGTTTAAAG TATCGAGCAT TTCATAGGAT TGCCTTATAG TTGGTCTAAT
14201 TTAACAACTG AAATAACCAG GCATAAGCAT AATTAACCCT GGACTCAAGA
14251 AGTTGAGTGG CAGCACCTCA GCTGTGGTTC AAAGCATAGC CACTACTACG
14301 CTTCTAAACA ATGGAATAAA GTATAAAGCG GTCTCTCAGT CAAGCCTCAC
14351 ACAGGTAAGA GGCGTGACTT TAAGGGAGTA AGATGAAATA TCGTAACATC
14401 ACCCCAGAAA TAATGCTCTC ACTTTGGTTA CTTTATTTGA TTAGTTGATA
14451 TTTGGCATAA GAGAAATCAC TTGTATTTCT CTATTTAACA ACTCTACATT
14501 TAGAACACTT AATTTTCTCA ATCCCCTAAA AAATTAACAT TTACTGCAGA
14551 TGTTTTCACA TTAACAGATT AATGTCTGGA TCATTCTGAA TTTTTGAAGA
14601 CCAAACATGT TAACATCACT GACATCACTG AAAACCAGCA ATTAATAGCT
14651 GTAACATTGA ATGGTACCTC ACCAAGCCAG CTAATCAGAA ATATCTCCTG
14701 TGTTCACACT CTGTAAGATT TAGCTTTAGC CAAGGTCTTT GCAAAGATTA
14751 ACCAAATAAT GTGTACAGAA GGTACATCCG CTATTGTAAA AATCATTTCA
14801 CTTTGACAGT ACAGAAGAAG CACCAGCCCT TCTGTTTTAG ATGTAGTCCG
14851 TCCTTTTCAA GCTGTATGAT TGTGGACATG TCAACTTAAC ATCTCGGAGT
14901 TTTTATATCT TCATCAGTGG AATGAGAATA ACAACATATA TCTTGTCATC
14951 TCACAGGGTT TTTCAGATGA TCAAATGAAG TAATGTGCAG AACTAACCAA
15001 TGTGGGGAAT TATTATCATC ACTGTTACTT TCATATGAAG TGAAGAAAAT
15051 ATTTTTAAAC TCAGTAGTTT AATTTACAAT TTAAGTATGT GTTTTAAAGT
15101 GCCTGTTAGC AAAAATTCAC TAGAAGGATG TAGGACACAC TTAAAGTTTT
15151 CATGTAAAAT TTGTGAGTTC TATTTTTAAC TGAATCTTTT GGCCATGTGT
15201 CAACAAATTA ACGTTATCCT TCACCAAATG GGTGGGCTTG AAAAAGGCGT
15251 GATGCATAAA TATTTACAGT TGTAGGCAAA ATTGTAATGT TATGTATATG
15301 AATACATATT CATTTTTTCA GGGAGAAGGC TTGTAGATTT CATCAAGAAA
15351 TCTTTCACAA GAGTAGATAA TCATTCATGT ATCACTTACC TAGATGCTCA
15401 TGAAATTTTG CCACTTTATA TAATTCCTTA GTTAGCCAAA AGGAGAGTAA
15451 GATGAAGAGG GGGGAAAAAA AAAACTTCTT TGACAAAGAT GGAGAGAAGC
15501 TGTCATCTCT TGTATTCTTT TATCAATCCA GGAAGCCTTT GGTTTTGACA
15551 ATAAGTGGTC TGAGACTTTG TGTACTCCTC AGATAGGTCC CGGAGGACTA
15601 GATTGGTGCC CATCTGCAGA AAACCAGAGG GGATATATTG ACTCTGCAGA
15651 TCTGCCCTTT GATTCTGCCA TCTCTCAGCT GGCCCATGCC TTTTGTTGCC
15701 AGACTACTGC CCAAGTTATA GACACTAACA CAGGCACACT GAGTATGGGC
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15751 TATGTTGATT TATAACTAAT GAGGGCAGAA CCTTAGAACT GCAGCTTCAC
15801 TGTAAACTTT GGAGCAGGAT TTAACACAGA ATCAGCCCTG ATACTGTTAA
15851 CAAAGGTCCA CCTGAAAGAG CTGGAAGGTC AAATGTCTAT CTTGGAAGAG
15901 AACTTGGAAG CAGTGCCAAA TACACAATGA CTTTTTTTTC CATTTGGGGG
15951 ATTAGATGTT CATCTTACAT ATCCCAAATG TCATAACTTG CTTGCATGTG
16001 ACTTCAGTAC TGTCCACACC ATTAAGCTGT CACATTTTCC ATTTTAGCAA
16051 TGTCAAGCTA CCTCTTTATC ATTAAATATG AACTACCTGA AGTAATCAGA
16101 GCATTCATGG GACTTGAAGA AAATACTGGG TATGTCTTAT GCTCCCTCTG
16151 TGACATCAAG TGACTCATTC TACTTGGTCT TTTCTGATTC TAATATCCCT
16201 GTCTCTCACT TCTAGAGAAT GGTACCTCAA TGGCAACTAC CTCATCATAT
16251 TTGTGTCTGT TGGAATTATT CTTCCACTTT CGCTCCTTAA AAATTTAGGT
16301 AAAGATATTT TCTAACTGGA AATATTTTTA TTTTTATTTC ACATTTAAAT
16351 AGGTTAGCTA ATTGTAGATG CCATATTCAC CTTCCAAAAT GCTTCTTCTA
16401 ACTTCTAGGT TATCTTGGCT ATACCAGTGG ATTTTCTCTT ACCTGCATGG
16451 TGTTTTTTGT TAGTGTGGTA AGTGATGTGA TGACATGATC CTTGCAGGTT
16501 GGTTAGCATG AGTTTTTTTG TGCCTAAATT AGTGTCCTCA TTTTGTTCAA
16551 GCACTTCACT AATATGAAAT AGTTCTTGTA TCACAAGTGA TTTTCTTGTA
16601 GACTAATTTA GAGCAAAAAA AGAGCAGCTA CGATTTAAAG ATAGTTGAGG
16651 TAGAATATCA AAGCTACTAC TAATGGTTTG GTCTAGGCAC ACTGGTTATA
16701 TATGGGGAAA AAAGGAAAAC TTCAAGCAGG AACATGACAA TAATCTGGCA
16751 TTTAGAACAG CAGAGGAGAG TCCCAGATGA GAAACAAGAA GGCTATATCC
16801 ATATTCACAT GAATCAGCCA TTCTCTCTTA CACATTCCAC CCATTAAGAG
16851 AGGACAAGAA CAGTGGGATT AAAGAAGAAA TCCTCCTCTC TAGGCCCCTG
16901 ACAAAGAGG GAATTTCTTG CACTATCATG AATGCCAAAA TTTATAAAGC
16951 ATTTCCCCAA AGAGGTAAAG GAGAAGGAAA AAAAGTTTTG AAGACCCATG
17001 TCACCTTAGT TTGAAGAAAT AAGGAAATGA TCATCTTTCT CATGGAAGGG
17051 CATGAAAGAG GGTGGGAAGG ATTCTTGCAA AATATTGTCC TGTTAACTCT
17101 AAGAGGCAGG GCTGCCAATC ACAGCTCCAA CTCTTCCCTT AGAACAGAGG
17151 CTAGAGGAAG TTTACTTTGT CCATTAGTCT AAAAGGAATC CCTAACTGAG
17201 TTCCCTCACC CCCCACCCTA TAAGCCACAC ATATGGATTC TTATTTCATT
17251 GTTTTTTCTC AAAAAGCTGA TTTTTTTTTC TTTTTTAATG ACTGAGTCTA
17301 GGTGATTTAC AAGAAATTCC AAATACCCTG CCCTCTACCT GTTTTGGATC
17351 ACAGTGTTGG AAATCTGTCA TTCAACAACA CGCTTCCAAT GCATGTGGTA
17401 ATGTTACCCA ACAACTCTGA GAGTTCTGAT GTGAACTTCA TGATGGATTA
17451 CACCCACCGC AATCCTGCAG GGCTGGATGA GAACCAGGCC AAGGGCTCTC
17501 TTCATGACAG TGGAGTAGAA TATGAAGCTC ATAGTGATGA CAAGTGTGAA
17551 CCCAAATACT TTGTATTCAA CTCCCGGGTA AGTGAGCGGT CCGGGCTTCT
17601 AATGAGTACA GTTATGTGTT TTCTAAGTTT TTATTCAATA AACTGAGATG
17651 GCCTGAGATC ACCATCTATG TTGGAATGCT AAACACGTGG TGTTGTCTTT
17701 GTTTTTCAGA CGGCCTATGC AATTCCTATC CTAGTATTTG CTTTTGTATG
17751 CCACCCTGAG GTCCTTCCCA TCTACAGTGA ACTTAAAGAG TAAGGCAGCC
17801 ATCATTTTAG CATTCTAATT TGCTTTGAAA TTCTGCTCAT ATGTTCAAAG
17851 ATTCTTTAAC AGGAAACACA GTTTATAGCT TCCTCTTCAG AGAAAATATG
17901 TACTCCATCC ACTCCTCAGT AACATGCTTT AATCAGAAAG GTGGGAATCA
17951 GCCCACCACA GCACTACCTT ATCTTCTTTC TCTCCTTTCT CTCCACCATA
18001 ATGGTTCAGG GGAGGGGTTC ATGGCAGGTG GACAAGGAGT CGATGGTTGT
18051 AATAATTTTG GCAGGTGTTG GGAATTTAAA TTTGAATTTT GTTCGGAAGA
18101 AATGATGTCA GCTGGACTAG AAATGAAAAC ACCCATGACG ACCAAAACTT
18151 ATGGTTAGGG GCAGCCTCGA TAAGCCAGTG ATGTCATTTA TAGTCAGCAC
18201 CTAACCCTTG TCTAGAACAC ATTCATTACA AGAGATGTGT CAATATCTGT
18251 CCTTTGTTGT CTTATTTGTA CAATAGAGTC ACTGGCTAGA AAATCTTGTT
18301 TCTTCCAGCT GATGGTCTAT GGTTCATTTG TATTCTTTTC CCTTTGAAGT
18351 TGTTGATATT TGCTTGGGAA CAAAGGATAT GAACTCATTA TAGCTGTTTT
18401 CCTCTTTCCT TTAAGGGAGG ATATTATATA ATAATTCTCA ACTTCTTTAA
18451 TCTAGACATC AGTAACCTCA GTCTTCATTC TCACTAAATA GCAAAACTTT
18501 CCCCATAAAT TCTGATTTAC CTCATAAAAA ATTTCAGAAC ACTTTCAAGT
18551 ATTTTGATGT CTTTGATTTA CTTTGAAAAT TACATGTAGC AGTTACTCCA
18601 GAAGCCTGAC AATTGATCTT TGGCAGCCAG GTTCCTTCTA GAATGGTTTT
18651 CAGAAGCTTT TCAGGTAGTC TGGACTCCTG GCAGTAGTAC TTTGCTGACT
18701 CTACTAGGTT CTTTTCCTCA TTTAAAGTCA TCTCATTATG AAATGCAAAA
18751 GCTTTCTATG TTAGGAGCCT GTTTCATCTT TATGTTAATT ATATTCTTAT
18801 TCAGTGGGCA AGCTTACTGA CCTACGTGAA ATAGACTGTT CCTCTTCTAG
18851 GGAAATGATT GTTTTTAAGA CTGAAGGACT AGTGTTTAAG AAAAAATGGAA
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18901 ATGAATCCTC ATTAGCTCTC TAAGACAAAT TTAAATCAGC TATAAGTTTA
18951 TGTACTAAAT ATGTCTTCAT GATTAGCAAT ATAGATATAC TTTTTTATTA
19001 TTATTTTCAT TTTGAAAAGT GATTTTTTTT TGTAAGTTTA AAAAACAAAG
19051 CTTGGTGTTC TTTCTTTTTC CAGTCGGTCC CGGAGAAAAA TGCAAACGGT
19101 GTCAAATATT TCCATCACGG GGATGCTTGT CATGTACCTG CTTGCCGCCC
19151 TCTTTGGTTA CCTAACCTTC TATGGTAGGT CACTCTGAAA GTCATTCTCT
19201 ATATGCAAAT CCTTGTTAGG CTGGTCCTTG ACCTGGGTAG GTATGATTTT
19251 TAAAAATTGC CTTCTATAAG CATGCTCTAT AGATGACACA TATTCAATTA
19301 ATATACTATT TTAGTTTTGT CACTTGACCT GAGGAAATGG GGCCTGATTC
19351 AGCCTGGCTA ACAAGTTACA AGAATTTGTG AATTAACACC TATTTTATAA
19401 AAAATATCCC TCAAACAAAA TTATTTTCCT CTAGGGATAG ATGATATTTC
19451 TCTGGCTAGA CTCCATAGTC CAACTCAGGC TACAAGTGAT GAGAATGAAT
19501 CCACTTGCAT GTGATAAAGC TCCTTTGATG GAATTATTAA CTGCCACACA
19551 AATAGCAGGG AAACTGCCAG GTCCTCAAGT TTGAATTTGC CTCCTCTTTA
19601 CCAGTCAAGT CAAATCTGGG AGCTTGGGAC TTTAGGTAAA ATTTCTGACA
19651 TATCCCATTC TATTTTGTTA TACTAAATGA TTTCCTAAGA AAGAGGACAT
19701 GACAGAATTT CCTTCAATCT AAGAATGCAC CACCAAAAAA AAGTGACTAT
19751 GGCCACATTA GATTATGCCT GCAACATTTC CTCTCTGGCA TCTTAACAGT
19801 TCACAAAGGG AGTAGGATTG TACTCCTTCC ATGAAGTGTG GCCACATAAA
19851 CAGATTTCAT GGAATCACAT ATTGACCTGG TAGCATATGT TTACATGAAT
19901 CAGTGTATCA ATATAAATAT ATTTTTGTAT AAACCTCCTT TTAAAGTTTT
19951 TAACTTAATT TTTTTCTTAC TGACTTGGTA AATTGAATTG CATGTATGAC
20001 AAATTGTGGA GGAAAAGATT CAGGAGTAGG CCACCATTTG CTTAGGTTTT
20051 TTTTCTATTT GACTAATATT TGACTATTAA CCAAACATGT GCTTTAGATT
20101 GGGCATTAAC TTTTTGCCGG TTGTGAAATA ATGAATGACG AGGTCAATAC
20151 TACTGAAGGT ATTTTCACTA CTTTTTTGTCT GATCTTGAGG TGAAAAATCCA
20201 ACTACGCTTG ATTCCATAGA TATTTTCTTG TTATTTGTGC TTGGAGTCCT
20251 GAATGAAGGT GTTTTCAAGT AGGGCTGCAT CTTCGTCTTA GAGTAGTACC
20301 CACTGGGAGA CCATCTAAAA ATTATACTAA TTTATCCCTG CACGTTACTT
20351 ATACTTATTT TAATGAGTTT CATAAGACAA GCAAAAACTT GAAAGAGCCC
20401 AAAAATATCT GTTTTAGTGT GGTGATGGAG TCATAGTTGT TGAGCTTGAA
20451 AAAATGGTAG CAATCATTCA TCCTAGAGTT TACACACTGG GTTTGTAACC
20501 TGCATCAGGA GTGGCTGCAC AGGTAGGGAC AGGGGAGGTG GTAGGCTGGG
20551 AGAGACAATA TGTGGGGCTT GGGTCTCTCA TCCCCTTCAA CAAGAGCACC
20601 TTGGTCTCTG TCTGATTTGT AATTGCTTCT GTACAGCGGA GATAGATTTA
20651 TCACAATGTA AATGAGCTTG AGAGGCTCTT TATTTTGTAT TATACCTTCT
20701 GCAACGTTAT CAGCTTCAGG ACCTCTTTGT TCATTTGAAT GAAGGTTGCA
20751 TAGCTAATGA GCTCAGAGGC AAGACCAGAG GTGCCTGGAT TCCCAGGCCT
20801 AGGTCTTTTC CTCTGTTCTG TGTTCTCTCT ATAAAATGTT GCCATAAGTG
20851 ACCTGTGCTG ATTTGACAAC ACCAAGCGGT TTCATTCTCT TTTTCCTGTT
20901 GTAGGAGAAG TTGAAGATGA ATTACTTCAT GCCTACAGCA AAGTGTATAC
20951 ATTAGACATC CCTCTTCTCA TGGTTCGCCT GGCAGTCCTT GTGGCAGTAA
21001 CACTAACTGT GCCCATTGTC CTCTTCCCAG TAAGTACATA AGACTTTGAT
21051 GAAAGAAACC TACTTGACCC CATAAATTAG TACATGTGTT CTACCTTCAT
21101 TTTGATTTAA TTATAGGGTG AGTTTGCAAT TGCAATGCCT GAGGATATTA
21151 TTTTCCTATA GCATTTTGAG TCACTTAAAA TTGGCCATTT AATGTGTAGA
21201 TAGAGCAAGT AGTTTCAGGT GGTATTTTTA TAGTGTAGGA AAAAAATCAT
21251 AAAACTTATT TTTAAACTCA AAGTTGAAAA GTGGAGCTGG AGCTTCTGTC
21301 TTGTGGATTA GTAAAACTGA GTAGGAGTTC ATATAACTTT GGAACCTTGA
21351 AAGCCAAAAC CATATTAACT TTCAAATCTT ATTAAATTTC ATCACAGTTT
21401 TGAAGGCATT TCATTTTTTT TCCAGTTTGT TGTGCTGCAA TAATATACAA
21451 AAGTTGCCTT TTTTAACCTG ATGCCTTGAA GGCTAATGAA AAGGGGATTC
21501 ATGTTAAGTA AATTATATAC CAGAAAAAAA TTTTTCAAAA AACAGTTATG
21551 CTATCTATCA CATATCTCTC TCACACATGG CCTCTGCCAG ACTCACACCA
21601 GGTCACCCCT CCCTGGCATT TGTCATTGGT GTCAGTTTGT TCTGAGATCC
21651 CAGAGCAGAG CTGGTAGTGA AGATTTGGGC TGTGTGAGTT AAAAACCACCA
21701 CCTAAGGATA AACACAGGTC TTCACCCTCC TGCCAGCTCC TGTTTCATAA
21751 ACACTGAATT TACTCATTCA TTTGAGGGGG AAAAAAATAA GTGACACAGT
21801 AACCAGCACT GTCCTGGACA TAATGTTCCA TACAGGGCTG GCATATGAAG
21851 ACTATTTCTA TAATGACACT GTGGTCACTT TAAATGCAGC TTGTGTGCTG
21901 AAATATATTT TGGCACATTC CTTTTTCATG AGTGCATGAA ATCAGATCCG
21951 TACTACTATG GTGGCTAATA TTTTACTCTT AAATCATGTC TTGCCTCTAA
22001 TATATCTGAA AGTATTTCAG ATGACATACA CATAGCTTTA GCCTAAAATC
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22051 AGCTCCGTCT TGGGTACAAG ACAGAAGACA ACTATAAACA GAAGGTATAC
22101 GATAGGGTAA AATTGCCAGG CAAACAACTT CACTGAGAAA AGGATATCTG
22151 GAGCCCTTCT TTTTATGTGT AAAAAAATCA CTCACTAAAT TTTGGCACAG
22201 TGTAAGCATT CACATCATTG TAGAATCAAA GCATAAGAAA TCTGTGATGT
22251 GCTTCTGTAT TGCTTTATTC ATATTCATAT AGTGTTTTCA AGCCATGGTT
22301 TTAAGGGATT GCCAGAATTG GCCATCGTCA CACAGACAGC TGGTAACAGT
22351 TCAACTAGTG CAGCTCATAG CCCAACACTG AGGGCTGCAA TTATTGTCAT
22401 GGGAAGTAAA AGTCATTTAC TGATGAACAT TTCACCTCAG CATGGAAAAT
22451 CCAAATCTCC CCTTAGAAAT TCTTACCCTA TGTGAGAAAT AAAGCACTGA
22501 TATAAATCTG ACCATCAGGA ACAGCAATAG TGTGTAAACA TTAGATGCCA
22551 TTAGAACCAA AATTGACCAT AAGAACCAGA GTTCAGAAAA ATGACTAACT
22601 GCTGTCCTTC ATTATGTATT TCCACTCAAC ATTAGCATTT ATGAAACATT
22651 TTGCACATTA TCCTGTCCTC ACCCTTGCAA TGTTACATTT ATATAATCTG
22701 TGTAAGTGCT CCACTGCCCC ACAGAGTCAT AAGTCCCTGG GACTTGGTGA
22751 TGTGCACAGT GACTGGCACA GAGGGTGAGC TCTGTCGTGC TTGGGAAGAA
22801 AAATGGTCTT CAAATGAATC TTGCCTTGTC TTGAAATGTA TAAACTGCCT
22851 TTTCTAGCAA AAGCATAGAC ACTCTTTCCC TTGGTGACAT GTGCTACGAA
22901 TTCAGCTGGG TTGAGGATCT GGGCTAAATG AACCAAACCT CCCTATACAT
22951 GAAGGATACA CAGAGATGGT GACAGAGAGT GGTCACTTCC GTGAGTGGAT
23001 CTCAATCAAG TCCTCTGAAG CTAAATTCAA TTTTTTTTCT TTACTAAAAT
23051 GATAAAGTT GTTATTGGCG CTTTTGCTTG TTTATTTCGT ATAACTTAGG
23101 GCTCAGATTT TCAATGTGTC AAATGCTGAC TCACAGCATG GTTCTCCTGA
23151 CAGTTTATTT CATTTAAGGA ACTCTTCACC AGTAAGTTTA TTTACTTGCC
23201 TTGATATCTC CACACATTAA TAATAAAACT AACAAAACCT AATCTGAATT
23251 AAAATCTATC AGCTTTAGGC ATTATTTTGT GTTCTCCTTC TTTCAACATG
23301 GTAACTGGGC TCTCTTTCTT AGGAGCTTGA GAAGATATGA CTGGGGTTTG
23351 TTTTTCTCTA CTTCATTTAT TATCTTTCTT TTTTCCAATC AGGTTAGTTT
23401 TTTCCTTTTT AGTAAAAGGT GCATAGTAAC TGCTTGTAGT ATTTGTTGAA
23451 CAAGTGAATA AATGAAATGA ATTAAGGTAG TGTTTTCACT AGCAGCCCAA
23501 CATTTCTTTC TCTCTTAGTA GTGGGTGGGG TATCAGTTAT GGAATGGCAC
23551 CTCCTTCCAG AGGACTGATC ATGTCATTTT CAGCTTATGC TTCCCTTTAT
23601 GCAGTAAAGT TTCCATATTT CCATAAAGAA CAAGAAACCA AATAATCCTA
23651 ATGGATATAT AATGAACACA CAGATGAAAA TTTCACCTGC CATGCCTTTG
23701 AAAAAGATC CCTAGCTACT TGTATTTCAT CTTATAATTA AAATCAGTCT
23751 TTTCACTTAT GTTTTCTTCA GATCTCCTGT TTTGAAGTGT ATATAGATAT
23801 CAACATAGAA ATGCAGCGTA TATTGCTATC AACTGCAGTG GAGCAGTGAT
23851 TCGTAGGTTT TCCAACATCC TTGCCTTAAG CAAACCTGCA AAATCAAAGT
23901 GTGAGCTACG TCTAAACAAT GGGAGAGGCT TTTTTTTTTT TTTTAAGAGT
23951 TAGAACTAAG ACTCTCACTT CCTCCTGTGC CTCCACATTT TTGACCTTCA
24001 CATTGGGCCC CTGCATCAGA ATACAGCACC CCCTAACAGG CTCCTGTTCA
24051 GGACTCTTTC TCTGGAAATA ACAGATGTTG TCTCTAGAGC TGCATAGAAC
24101 CTTAATGGAA TCATTGTGGG TCAGAGGCCC TGGATGGTGC TGGGGACCTC
24151 CCTGACCCAC AGCATCTGAC CCACATTTCC AGGTTCCTAG CGACTTGTGT
24201 CAGTAAAGAA AAAGGCACAT AGCTAAGTGG AAGAGCAGAT GAGGCTTGGT
24251 GGGAATCAGC CAGTGGTCTG CCCTAGCAAA GGTAAACAGA ACTGCTGGGG
24301 GCTTTTGGTC CTAGGCTCAC TACTCAGGGA GGCACTTTAA CATGGAATGA
24351 CCAGCAAGTT TCCTTCCTGA TCTTTTCCAC CACCACCACA AGCCTAGTAC
24401 CTCCCTCCCT CTTTGCTCTG TTGCTCTCTT CGGGAATGCA CTGGAAACCA
24451 CCTTCAGTTC TGTTTGGAAT TTTCCTATTC CTTATTCAGA AAGAGGAAGA
24501 AGCTTTTGCA TTTACTCCAA CCGTTCTACC TATTATTCCC ATAAACTTTC
24551 TGTGATCTCA TATCATTAGG CCAAATGTTA ATCTTTCTGG GAGCCAGGAG
24601 ACTGCTTTCA CATTCAGAGG CCCTGGACAT ATAGGACTGC CTCTAACTCA
24651 CTCTAACTCA GCTTATTGAC TTGAATGCAC CTTTTTAACA AGTGACTAAA
24701 AAACAAACTG TGACTATTCT CTGAAAATGA GCCTATATCT CATACTTATT
24751 TATTCTGTTT AACACTGTGA AACAAATTAA GTCCTCTGGC ACTATGTATA
24801 TACCATAAAA AGCTTATTTG TAAGCTACT AATTGGACCA GTTTTGACAA
24851 TATTGAATAA GCACTAATTG CAGATCATAA TGTAGAATTA TAGGCTGCTG
24901 AGGAAAACAA TATCACACCA TTTGCTTTCC TCAGTTTCCT TTTCAGAATG
24951 AGTTTCATAA TGTTCACTAA TCCAATTTTT AAAATCCTTT ACAAAGTTAT
25001 TCTTAAACTA TTTCCAGAGA CTATCTGGTT TGTCATTCTA GAAATGAAAT
25051 TGCCTTTTCA GCCTAAACAG ATGGCCTTAA TTTTTGGTGG AGTGGTATGA
25101 AAGGAATGTC ACATGAGAAA CTGCAAGCTA TTTAGCTTGA ATTTTTTGTC
25151 ATTCATACAT GTTTCAAAAT ATATTTTACA TTTTCTCTCT TTTAAATGAG
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25201 TTCCCATCTC TGCACCTTAA GTGACTTCAG AACTAAAATT TTAAAGTGAA
25251 CATCAATCAC AGCATTTCCA AAAATGTGAA CTCCTAGCTT AACCGAAGTA
25301 TTCACTTATT GGAAAGCTGA TAGAGTAATT CCACTAAGTC CAAAAAGTGT
25351 CCTCTAAAAG ATTCCAAAGA TAAGAGTGTT TTCAACTTTG TCAAGCTGTA
25401 CAAACACAAA TGTCACTCCC TCCCTCTGCC CACAGGGATC TTTATCCAGT
25451 TACAGCAGCG TAACTTGAGC AGCTGCTGCA AACTGAGGCT CTCTTGACCC
25501 TTCGCCTACT TATTTCAGCT GCTAAAATAG GGCTGAAATC TGTCAAGGAT
25551 CCTGAAGGGA AGGATAAGAT TCCTACTATT CAATTTAATT TAAGCTTTTA
25601 TTCAGTGCCT GCTGTGTGCA CAACACTAAG CTAGAAAGTC TGAGGAATGT
25651 TTAGATTATT AGGTCCTGTT CCTTGCCTTT CATAGATTTA CAATCTATTG
25701 ATAGGGAGAG CTAAAAAGGA GAGAAGAGG AAGGAGCAAA CATAAAAACG
25751 TCAAAATTTT AAAATACCAT TTTAAAATTT TATTTTAAAA TGTTAAATAC
25801 CATGCAAAAT TAAGGAAAAC CTAGATTCAT AAAAATTCCT TTCACAATCT
25851 TGTGTAAATC AATTCAGTGC TTGCCCTTAA TGTCTCATCC AGTCTGATGA
25901 GACATGTTTT GTGATCAACA AGGGTTTTAC TATGTTTCTT AATTATGTGT
25951 CTTGCCTGTT ATCTCTTTCT GACCGAGATT ATTTTTAACA ATAAATTCTG
26001 AAAACTAAGA AAGTGAAAGC ATAAAATATT GTCTTATAAA ATACGCCAAG
26051 GAAAAAATGA CACTCCATTT CAAATATCAA AAGTTAGCAT CAAGACTGCA
26101 CAAGATGAAT GTACAGTCAT GTGTTGCTTA CAAATGTGGA CATATTCTGA
26151 GAAATGCATC TTTAGGCAAT TTTGTCATTG TGCAAACACC ATAGATTGTA
26201 CTTGCAGCCT AATTGGTGGA GCCTACTATA CACTAAGGCT ATATGGCATA
26251 GCCTAGTACT CCTAGGCTAC AAACCTGTAC AGCATGTTAC TGTACTGAAT
26301 AGTGGAGGTA CCTGTAACAT AATGGTAAGT ATTTGTGTCT CCAAACGTAG
26351 AAAAGCTACT GTAAAAATAC AGTATTACAA CCTTAGGGTA TCACTGTCTT
26401 ATATGTGGTC TGTTGTTGAC CGAAATGACT ATGCTTAATA CCACTGAACT
26451 GTACACTTAA AAATGGTTAA GATGGTAAAT TCTATGTTAT GTATGTTTTA
26501 TAATAATAAA AAAATTGAAA AAAGCATCAA CATCTTTTCT GGGAAAAAAG
26551 AAAAAGAAAG AAAATGCATT AGAGTGATGA GAATATTTGA AGTAATAGAT
26601 AAAGTCAAAA ACAAAGAAAT GATCTTGCCT TTGAACTTTC TTGTTTAAGA
26651 TTCGTACATC AGTGATCACA CTGTTATTTC CCAAACGACC CTTCAGCTGG
26701 ATACGACATT TCCTGATTGC AGCTGTGCTT ATTGCACTTA ATAATGTTCT
26751 GGTCATCCTT GTGCCAACTA TAAAATACAT CTTCGGATTC ATAGGTGAGT
26801 TTCAGAAAGG CTTCAATTTG GTCAACCCAA ACTCACGCCT CATTAAATGA
26851 TGGACAGGGA ACCAGTGCTG GGTCATCCAG ATCCCCGTTC TTTCTCAGGC
26901 TCATGGATTC CCTTTATCCC TGCGAGGCTC TGGTGATTGA GCTGCTCACT
26951 GTCTCTTCCT CCTAACTGAC ACTGGGAGCC ACCTTATAGG TCATTTAGTC
27001 AAGCTGCTTT TTCTGATAGA TGAGGAAACT GACCCCTATA AAAGTCAAGT
27051 CATATACCTT GGTGTGGACC CAGGATTTGG ACTTAGGTAT TAGCTCCACC
27101 ATCAGGAAAA GAGGAAGATA GATTTTACCT GCCAGAAGCT CTCTGATACT
27151 ACGAGTATCA GCTGAACATT GAAAGGTATC TTCAGAGGAA TAGGAGGTTG
27201 ATTATATAAA GTGTATTATT AGTATTTCCC CATAACTGCA TGGTCTATTA
27251 ATTTTCATTC TACTCATTGA GGGTTTACTT AAACTTTAAA CACAATCTAA
27301 AACTTTAAAA GAACCATGGG TAGGTCACTT GCAAGTAAG AGGTGGATAG
27351 GGTGTGTCAT GAGTTCAGCC ACCTTAGTAT GTATTTATAT TACTAATCCC
27401 CTGTAAATTT GTGTTAAATT CAGCCTTTTG TTGCTTATTA TATGTTGCAT
27451 ATACTTATGC AGCTTTGATG TTAGGTACAT TTTAATTGTC TCTATAAACA
27501 TATCTTCTAT GAATAAATAA CCAAGATGAG CTTATGTGAC TTAAGTGTGT
27551 GTTTTTAGTG CTAAGTATAG GATAGCTTTA TATTTGGTTT ATTTAAAGTG
27601 TGTGCTGGCA TCTCCTTTGC TAGGAACTGC TGGGTAAGAC ATTGACCTTG
27651 CCCTGTGTTT GTCTTCTCAG GGGCTTCTTC TGCCACTATG CTGATTTTTA
27701 TTCTTCCAGC AGTTTTTTAT CTTAAACTTG TCAAGAAAGA AACTTTTAGG
27751 TCACCCCAAA AGGTCGGGGT AAGTAAACCT TGCAATTTCC CCCATTATTA
27801 GTTGTTCTTC CAACTACTTA GAATAAACTA GAAAATACAC ATAGTTCAGA
27851 AAAATGAATC AATGTACAAG AACCAAAAAT CAAAAATGGG CTAGAACTTT
27901 CTGGTAGCAG AGAAAGGGGA CATATTTCTG AAACTCAAAT GATTCTACTT
27951 CAAATATCAA ATATCCTGTG TTGAGTCTGT CATACATGTC AAATAGTAGT
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28051 CAAGCTGCTG TTGTGCTATC CGTGGAAAAT CATGCAAGAA GGAATTAGGC
28101 TCCCTAGCGG TGTTATGGAA TAATTTAAAT ATTTTGGTCA TGGTTGTTAG
28151 GTTTGCAAAG CCAAAGGAAA GATGTTGCTT TTGTTTTCCC TTCCATAGTA
28201 CCTGTTGTCC CTGGTGTGGA CTAAGATCCA GAACAGAACC ATTCATCGTT
28251 CTGTTAACCT CTTTAGATAC AAAATACAGT CTTATTAAAT TAGAGAGTAC
28301 ATATTTCTTT TCCATAAGAC TACTATAGAA ACAAATGCTA GAAATAATTG
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28351 TTTTTCCAAT AAGGAAATAT TATCTTTCAC TCCTTAATAA AGTCATGTTA
28401 AGGCTTGAAA AGAATATTTC TTACTGAATT ACTCTGAATT TTTACCTTGA
28451 AGTCATTTAC CTTTGGGATG TTCTGGGGAC TTCAGGATAA TTTGGTATCA
28501 AAAGGTCCAC CCAGCAGCTT GCTCCCAAAT TTTAACTCTA TGTAGTCCGT
28551 CTTGCTTGGA TTTTTACAGC AGTGTGACCT TGGCAAATTA CTTGTCCTGT
28601 TTGTGACCTA TTTTCAGTTT GACCAATTGT GAAATGAGTA CAATTATCTC
28651 CTAGACCCAT TCTAGTGAAA AATGTTTAGT TGCTGCTTTC TTATATGTAG
28701 GATTAGGAGG TTTAAGTATG TGATAAAATG TAAGGCCTCT TCTGGTGTTA
28751 AAATGCTGAA GTATTTTATA TGTAGGTATG TACATATATC CTTATATATG
28801 TGTGTGTATA TTATATGTAT GCACACACAC ACACACATAT ATACACTTTT
28851 TGTTGCAACA TCTATTAAGC TTTTGGTTTT GTTTGCTTTA TAAAATTAGA
28901 ATCATATCAT ATATGCTATT CTTTTTTAAC CTGCTCTTTT TCACCTAAAA
28951 GATTGTAAGC ATTCTCTAGA TTATTGAATC TTTTTCTGTC CCTTGATTTT
29001 TAATAATCAC AGGGTATTCC ATCATCTTGG TGTACTAAAT CAATTAACTA
29051 TTACTCCATT GTTGAACCTG TAGGTTGTAT CTCTCCACTG TATTCCTCTT
29101 CTTTCTTCAA CTAGGATTCT AAATTGACTG ATAGGTTAGG CCTGGGCATC
29151 TGAGATATTA AGAATAATAT GGCTCAATAT ATAGATCAGA TTGCCATATT
29201 ATGTAAACAA CTAAAAAACA AATTGTACTA AGTATGGTTT CTGTGCTCCT
29251 AACAGAGTCT CTCTGAATTA CAGGCTTTAA TTTTCCTTGT GGTTGGAATA
29301 TTCTTCATGA TTGGAAGCAT GGCACTCATT ATAATTGACT GGATTTATGA
29351 TCCTCCAAAT TCCAAGCATC ACTAACACAA GGAAAAATAC TTTCTTTTTC
29401 TATTGGAAAT GGTTACAAGT TATACTCCAA AAGATATTTG AATTATCTTG
29451 ATTGGAATGT TATTCATAGG AAATAACAGG AAGATTCCAA AGACGTTTAC
29501 CAGTAATATC ACCAGGCACC TGCAGAAGAG GAAAATCACT GTTTTTGTCA
29551 AGGATGGTTG TGTATGTGTT TAAAATAAAA CCTGTGGTGC ACATTTCTAC
29601 CCAGGTTTTG CTAGAGCAGT GTGAGATGAT GAAGGTGTAT TTTTGCTGCT
29651 TTACGAGCAG AATAAGGGTA ACTGCATGTA ACAATCATCA GATAGTACTC
29701 TTTCCCCTGC CGTCTCCTCA TCCTGCACCC CCTAAAAAAG TACCAAACAT
29751 TTGCATTCTC AGAACATCAA ACAAAAATGC CCTGGTGGCA AAGCTATCAC
29801 CATTTAATGT CTTCTCTCAG TCTTGCACCA AAGTCTCTGG TCTGTTTACT
29851 AACAGAGGCA AAAGGCATGT CTTAGGAACT GTTTCTGTTT CTGTAAGGTA
29901 CATGAATGGT CAAACACCAG TCTAGAGCAT CTTATTGTCA ACAGCAAAAT
29951 AATATTTTGC CCACCCTGTT TGTGACATTG AGTTGTGACT TCTATATTCA
30001 ATAGATTTTT GTAAATGTTA AAACATCTAT ATTTAAATGT TAAAACACTA
30051 AATATAGAGA GGGGCTTTAT TTCAATCATA GAGCAACAAC AAAAATAATG
30101 CTTATAGCTA AACTGCCTGT TCTAGAAAGC ATCTGCTTTT TCATGTTATT
30151 CCTAAATCCT CTTGTCATAC TTTTGTCATT GAACAATGCT CTCCCTCTCG
30201 TCTTCCATCC TCATTCAGAA TTTTTAGAAG ACCACAATCG TGGAGATACA
30251 CTACCCAGTA TTGTTTGATA CATTTTTATT TGATAAACAT TCAGTGCAGG
30301 AAACTGTGAT TTGCTATATG TTTATGTATA TAATCTTATT CTGTAGTCAT
30351 CAGAATGTTA ATGTAAGGTA CATTTGATTT TTATTTTTTA CATGTGTAGT
30401 TTTCTTTCTT CACAGTCAAA GCATTTATAT TATTGGGGGT GGGGGCAGGG
30451 AATTAAGTTG GTGGGCTCGA AAATCCATTC ATATGTATCT GTCTACAAAT
30501 GTCTGGGGAT AATTTAAATT TGAAACCTAA GTTATATATA GTTTGGCAAT
30551 GCTCTTCTTC AATATTTACA ATAATAGGAT GATCTACAAG AAAATAAGTT
30601 TCTTTTTGCA AATTTTTATC ATACTAAAGT TGTTCTTTTA ATTTAGCATA
30651 TCTAAAATAG GAATTAGTTC AGTTTAGCTC ACACAGGTGT TTGCTGACAT
30701 TCATTGGCCA TTTAATACAG TGTTGAGTGG TTCTCCGTAA AAGTATAAGT
30751 GCTAACACTA CGAAGAAATG CACACGATCA TTCTTGCTCA CTTCTATAAC
30801 AAACTTACAT AAAATGGATT TAAAAATTCC TACTCACAGC CTAAAACTTC
30851 TGGAGTTCAC TACCTTTTTT TCAAATCATA GTAAGATCAC TTGTGTATTT
30901 TATATTTTAG TAAAGCCAAT TATGAAGTAC AAGTATCATA CACGTACTTT
30951 TGAGCTACTA TTATTGAAA AAAATCTGCC AAATAGCATC TTTAGGATAT
31001 ATTTACATTT TCACTCATCT AAAAAGTATA CAAAAATAAA AAGTGGAAAA
31051 AGGTATCTTC TGAATGTTCA AGAGCATCCT ATAGTGCCAA ATAATAAAGC
31101 ACCATTTTTT TCTTCATAAC CAGGATTAAA ATTCATATAT ACTGCAGGGC
31151 AGACATACAT ATGATAGCTT GTGCTGATTA ATTTAACCCC ATTTGTAAAC
31201 AGATGAAAAT TTTATTTTCT TATTTCATTT ATAAGATGGC TCAATGTATT
31251 GGGAGGCTTC TTTTTTATTA CAGAAAGTGT ATATTGGTAT ATAATAAATG
31301 AACTTTTCAA ATGACTATGA TGTGATTTTT GATCTATTGT TAAAGAATGT
31351 TGTGTTATTT GTCCATGAAA CAAAATTTAA AATCCAAATA CTGTCTTTCT
31401 TATATTGGTT TATGTTCCAT TTTCATTGTT ACCTTTGACA CATAACTAAC
31451 ATCTATAGCC ATCATCCTGA AAATAATTGC CATCTTATTT TGGCAAAATA
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31501 GATATTTAAT CCTAAATTAT TATGATGATT ATAATTTTGG CATCACATAT
31551 ATACCACCTA GAATGAATGT GGAAGAAATG AGTCTTTTAT GGTTAGTTTG
31601 AAAGAATCCA TTGAAGATAG AAAATGAGAG AATAGAAGAA ACCTGAGAAT
31651 AGTAAAATAA AGAGCAGAGA AAATATGGGG GCAGGGAAAA CATGTGAGTG
31701 CTAAGGATTG ATTATGAATG AACGATTAGG GGGATTGATG GATCACAGGG
31751 TAAGTATATG CTTAACTTTA TAAGAAACTT CCACATAGTT TTCCACAGTG
31801 TTTCTACCAT TTTCATTTCC ACCCGTACTA CCTACAACTT CCACTGACTC
31851 CACAGCCCTG CCAACATTTG GTGTTGTCTT TTGCATTTTA GCCTTTCTAG
31901 TGGGTCTGAA ATGGTAACTC ATTGTGATTT TCATTTCTGC TTCTGTGACA
31951 ACTAATGTTG AAAACTTTTC AAGTGTTTAA TGGTCACTCA TATATCTTCT
32001 TTTGTGAAGT GTGTATTCAA ATCTTTTGCC CATTTTTAAA ATTTAGGTTA
32051 TGTGTTTTTA TTGGGTATTT GTAGAAGCTC TTTAAATATG GATCCATGTC
32101 CAGATTGCCA ATATATTTTC CCAGTCTATG GTATGGTTGC TTATTTTCCT
32151 AAAGGTGTCT TAATTACATC TTTCTGGGGC CAGGTCACCA TAGCTCAAAG
32201 TTTTGCAATT TATGTCTTAA TGAGATAATA TTAATCAGAG TGGTATAGTC
32251 AAAATTAAAT GTTTTGATGT CCTGGGCCCA TATAGGTAGG ACTGGATCAT
32301 CTAACCAAGA TGCAAAAAAA AAAAACAAA AAAACAAAAA TAGTACTTGG
32351 AAAAACTTAT TTTAAATTAA ACA
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FEATURES:

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Start:   3000
Exon:    3000-3118
Intron:  3119-7452
Exon:    7453-7543
Intron:  7544-8039
Exon:    8040-8155
Intron:  8156-10894
Exon:    10895-10968
Intron:  10969-11437
Exon:    11438-11530
Intron:  11531-16047
Exon:    16048-16129
Intron:  16130-16215
Exon:    16216-16298
Intron:  16299-16408
Exon:    16409-16467
Intron:  16468-17301
Exon:    17302-17577
Intron:  17578-17709
Exon:    17710-17789
Intron:  17790-19073
Exon:    19074-19174
Intron:  19175-20904
Exon:    20905-21029
Intron:  21030-26649
Exon:    26650-26794
Intron:  26795-27670
Exon:    27671-27768
Intron:  27769-29273
Exon:    29274-29372
Stop:    29373
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CHROMOSOME MAP POSITION:
Chromosome 12

ALLELIC VARIANTS (SNPs):

DNA Position	Major	Minor	Domain	Protein Position	Major	Minor
1386	T	C	Beyond ORF(5')			
2594	T	C	Beyond ORF(5')			
2757	G	T	Beyond ORF(5')			
6107	C	T	Intron			
6392	T	C	Intron			

FIGURE 3, page 11 of 23

9484	C	G	Intron			
10280	A	G	Intron			
10297	G	A	Intron			
10331	G	A	Intron			
10536	T	C	Intron			
11548	T	C	Intron			
11917	G	T	Intron			
12840	T	–	Intron			
12844	A	–	Intron			
12847	T	–	Intron			
13019	C	–	Intron			
13022	A	G	Intron			
13285	G	A	Intron			
14461	G	C	Intron			
15464	–	G	Intron			
15469	–	A	Intron			
15545	T	C	Intron			
16199	T	C	Intron			
16798	T	C	Intron			
18103	C	T	Intron			
18421	A	G	Intron			
18528	G	A	Intron			
18722	T	C	Intron			
18775	C	G	Intron			
18951	T	C	Intron			
18974	T	G	Intron			
19540	A	C	Intron			
19841	G	A	Intron			
20170	A	C	Intron			
20343	T	C	Intron			
20519	G	A	Intron			
20963	T	C	Exon	411	P	P
21840	G	T	Intron			
22783	C	T	Intron			
22787	G	A	Intron			
22825	T	C	Intron			
22967	A	T	Intron			
23248	A	G	Intron			
23764	G	T	Intron			
23765	C	T	Intron			
24432	A	G	Intron			
24538	C	G	Intron			
24693	T	C	Intron			
24819	C	T	Intron			
25743	C	T	Intron			
26044	G	C	Intron			
26555	G	A	Intron			
27886	A	C	Intron			
31884	T	C	Beyond ORF(3')			
32229	T	A	Beyond ORF(3')			

Context:

DNA
Position
1386   ACCCATATGCATGTCTTACTTCTATTCTCTCTTAGCTTTTAACCTGCTTCTTTTCATCTT
TTATGTATATACATTTAGGCTGCCTTATATTAATAATAGTTTCATTTTTGTTCCTCCTGC
TTAAAACACTGTGTGCTATTTTTTTAAATTCTGAGAACTGCTTTCTTTATTTCTAGACAA
TTCTCTGCCATTATCTCTTTCTGTTTTGTCTCACCCTAGTCTCACAATTCTCTATATTGG
AATGACTATCAGTGTATATTTGAACTTGTAATTCTTATTTTTTCCCCATTCCTCTTAACT
[T,C]
CTTATTTGTATTTTTCTTTTTTTTAATCTCTTCATGCTATAATTTGAGTGATTTCCACAGA
TCTGTCTTTCAATTTTATAAGTCTTCCTTCAGCTGAGTTTTTTTAAATTTCAATGATTCT

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              ATTTTTTTCTTTTTTTTTAAGAATTCCTTTTTTTTGACTCTTTTTGCAACAGCCTGTTCTCC
              TTTTATATTCCTTTATAATGTTTTTATTCTGTGAAAGTTATTCTCTTATTTTGAATGTTT
              TCTTTCAAAATGTCTTTCTTTTTATTAATTTAATGTAAAAGTCCCTTTTAAATTGCTTTG

     2594     CTGAACTTTCTTTTGTTACTATTCTTAACTTTGGCTTCAGGATCCAAGTGCCTAGAAAGT
              TACTTCCTAAACTTGATCCTCACCTATGTTGCATATTATCAAGCATTTGGTGGTGTTAAT
              TCTTTCATGTCCAATTAAATTAAAGCAGTAATTTTCTTTCTAGTTATTGCTAGTAGAGAC
              ACTGGTAGATTCTGCCTTGGTAGACCTTCCTCTGTCAACAATTTACTTTTGTCTTCCTTT
              CTTTTAAAACATGTATCCCACTCACAAATACCTAAATTTCCTTGAAGACTGCTGCCATGT
              [T,C]
              TTAAGATTTCTTTTTTTTTTCCATAGTGACTAGTAAAACCTGCCATTTTCATTATACATAG
              GCACTCTATAAATATCTGCTAATTTAGCAATTATTAGTAATTTCCTTTCTTCTCTTCCAT
              TTCTTCCTTTCTTGTATTGGGTAAAGGAACATTTCAGGATTTGCTTATGTAAAGTTTTCA
              GGAGTTTCTTTCCTTCCTCCCTTTTACAGAGAGCATACAAAATGTAGATGATTCATATTC
              ACTTATTTCATTTAAATAAAATTATAATGATGTATGTTGTGTTCTGTTTGCAGAACAGAG

     2757     TTATTGCTAGTAGAGACACTGGTAGATTCTGCCTTGGTAGACCTTCCTCTGTCAACAATT
              TACTTTTGTCTTCCTTTCTTTTAAAACATGTATCCCACTCACAAATACCTAAATTTCCTT
              GAAGACTGCTGCCATGTTTTAAGATTTCTTTTTTTTTTCCATAGTGACTAGTAAAACCTGC
              CATTTTCATTATACATAGGCACTCTATAAATATCTGCTAATTTAGCAATTATTAGTAATT
              TCCTTTCTTCTCTTCCATTTCTTCCTTTCTTGTATTGGGTAAAGGAACATTTCAGGATTT
              [G,T]
              CTTATGTAAAGTTTTCAGGAGTTTCTTTCCTTCCTCCCTTTTACAGAGAGCATACAAAAT
              GTAGATGATTCATATTCACTTATTTCATTTAAATAAAATTATAATGATGTATGTTGTGTT
              CTGTTTGCAGAACAGAGTGTTCTGAACATCAACACAAAGTGGAAGAACCTTAAGCTGAAG
              GTACAGTATATTATTTACACTGAAGGGGCTTGTGTGTGGACAAGAAAGCGCTGACAGCTC
              AAATGGATCCCATGGAACTGAGAAATGTCAACATCGAACCAGATGATGAGAGCAGCAGTG

     6107     GTTTCGTGTGCTGTTTCTATCTACATCTCATACTGTTTTCTATTCTCAAAAAGTAACCCT
              GTCATCCTCTTTCCTCTCCAGATTATTTTCAGGATTAGCTTCTGTTATAAAAAATAGCTT
              GTACAGATCTCCTACAATAATTATTTTCTATTTTATTTCTAAGGTTTATTTATTTATTTA
              TTGAGACAGACAGAGTTTCACTCTTGTGGCCCATGCTGGAGTGCAATGGTGCAATCTCGG
              CTCACTGCAACCTCTGCCTCCCAGGTTCAAGCGATTCTCCTGCTTCAGCCTCCTGAGTAG
              [C,T]
              TGGGATTACAGGCGCCTGCCACCACACTCGGCTAACTTTTTGTATTTCTAGTAGAGACGA
              AGTTTCACCATGTTGGCCAGGCTGGTCTTGAACTCCTGACCTCAAGTTATCCACCCACCT
              CAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGTGCCTGGCCTCTAGGATTAT
              ATTAATAGAACAATCTTCAATTATTTTATCTTTCTTTATCTTTCTTTTCATGTAGGAAAT
              GTCCTAAAATTTTCAAACCCTCAATTTGAAAGCACTTTTAAAATCATACATAGTCGAGCA

     6392     CAGCCTCCTGAGTAGCTGGGATTACAGGCGCCTGCCACCACACTCGGCTAACTTTTTGTA
              TTTCTAGTAGAGACGAAGTTTCACCATGTTGGCCAGGCTGGTCTTGAACTCCTGACCTCA
              AGTTATCCACCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGTGCC
              TGGCCTCTAGGATTATATTAATAGAACAATCTTCAATTATTTTATCTTTCTTTATCTTTC
              TTTTCATGTAGGAAATGTCCTAAAATTTTCAAACCCTCAATTTGAAAGCACTTTTAAAAT
              [T,C]
              ATACATAGTCGAGCATTTTATATAAAAACAACTAAAAAGTCTGTGACATTTTGCAGTATA
              AAAATGCAATGGCAGCAGCAGGCCTTATTAATTGAGCCTCTTGGAAATGTGGCTGGTCCT
              AGGTCCGTAGCCTCAAAGGCCCTGGCTTGTAACTGCAGGAGCTGACCAGCACAGCTCTAT
              AACCAAGTTGTACATCTTCTAGCCTGTGTCCAAGAAAACCAGAATCACAACGCTCTGTGG
              ATAGTGACATCTTAAAGTTTTCTTTCCCTCCCAACTCTTTTGCCAGTTCATTGAATTGCT

     9484     GCAACATTTATATCACAAATATGTGCTGTTTATGTTCTGAATATCACATATGATTAGTAA
              TCACACAGCTATTTGAGGGCTAAGCATCAGGACTATAAATATTTGTATTGTGTTAGTGCT
              TTGATTGAACTCTTTTATGTATAATATTCTTCAGCTGAATGGGTTTTTATATCAACTTTA
              CTTTTATATAAGCCATGTTTTGAAATAAACTAGGATTTTAATAATCTGAATTTTAATAGC
              TATGTATGTAGTCATATATTTGTATGCTTTTGTAATGTGCTTACCTCTAAGACAAAAAAA
              [C,G]
              CTGCCTTTCCTTATTAATTATACATACCATTAAAATGAATTAGGAAGTTACAGATCACTG
              ATGAATAGAAATAGGAAAAACTTCCCCCAATCCCACAGTCATAGATCATCTTCATGAGAG
              AAGAATGTTCCACTTTTTAAAATGAGGGCCTCATTTTAGGCTTATAAACACTTAGCAGAT
              GAATTTGGTCAGAACAATTAAATCACTAAACATCATGGGGTGTGTTTGTGTGTCTAAGT
              AGCCCAGACTGGATTAAGCTTTCTCTCTTAATTTATAGCAAGTGACACAGTATTTTAAAG
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FIGURE 3, page 13 of 23

10280   ATAAGAGTGCAACATAGCTACAGGGGGTTATAAAATTTATAATTCATGGTCCAAATGTACA
TTTGTAGTATTGATTTCATTGGGAATTACCAAGGGATTAGATCAATTGTGGGGAAAGTGT
ATTTTTTAAAAATAAACAAAGATAAAGATTTTTTTTCTGAATTCCAGGTAAAAGGCAGCA
TTGCTCCTCCATTTATTACGTAGATGCTTCTATCAACATTCTTATTTTTGTGCTCCAAAT
CTTGGATTTGGAAAAATACCAATCCGTATAAACATAAAGAAACCATACATGCATGTGGGG
[A,G]
TCCTAACACCAGAAATGACTCTGAATGCAAAAAAAAAAAAAAAAAAAAAAAGGGAATTTTC
GTGCCCCATCCTTAGCTTTCTCTGCTTTCTCTATTATATATGCAACTGCCTGCCCCTCTA
TCTTACAAAGTACTTCGTAATCTAATGCACAGGATCAGCAGTAATGCAGCTCAGACTGCA
TGCTTTCGCCTTTGGATTCCTAGATTTCAGATTAAGGTTTAGTCAGGCTATTGAATAGCC
CTTCAATTCTAAGTGCTGATGTGAATATCATGCAAATATGATGTACATATTCCCATGTGC

10297   CTACAGGGGGTTATAAAATTTATAATTCATGGTCCAAATGTACATTTGTAGTATTGATTTC
ATTGGGAATTACCAAGGGATTAGATCAATTGTGGGGAAAGTGTATTTTTTAAAAATAAAC
AAAGATAAAGATTTTTTTTCTGAATTCCAGGTAAAAGGCAGCATTGCTCCTCCATTTATT
ACGTAGATGCTTCTATCAACATTCTTATTTTTGTGCTCCAAATCTTGGATTTGGAAAAAT
ACCAATCCGTATAAACATAAAGAAACCATACATGCATGTGGGGATCCTAACACCAGAAAT
[G,A]
ACTCTGAATGCAAAAAAAAAAAAAAAAAAAAAAAGGGAATTTTCGTGCCCCATCCTTAGCT
TTCTCTGCTTTCTCTATTATATATGCAACTGCCTGCCCCTCTATCTTACAAAGTACTTCG
TAATCTAATGCACAGGATCAGCAGTAATGCAGCTCAGACTGCATGCTTTCGCCTTTGGAT
TCCTAGATTTCAGATTAAGGTTTAGTCAGGCTATTGAATAGCCCTTCAATTCTAAGTGCT
GATGTGAATATCATGCAAATATGATGTACATATTCCCATGTGCTGAGTAAGTAGATGTAG

10331   AAATGTACATTTGTAGTATTGATTTCATTGGGAATTACCAAGGGATTAGATCAATTGTGG
GGAAAGTGTATTTTTTAAAAATAAACAAAGATAAAGATTTTTTTTCTGAATTCCAGGTAA
AAGGCAGCATTGCTCCTCCATTTATTACGTAGATGCTTCTATCAACATTCTTATTTTTGT
GCTCCAAATCTTGGATTTGGAAAAATACCAATCCGTATAAACATAAAGAAACCATACATG
CATGTGGGGATCCTAACACCAGAAATGACTCTGAATGCAAAAAAAAAAAAAAAAAAAAAA
[G,A]
GGAATTTTCGTGCCCCATCCTTAGCTTTCTCTGCTTTCTCTATTATATATGCAACTGCCT
GCCCCTCTATCTTACAAAGTACTTCGTAATCTAATGCACAGGATCAGCAGTAATGCAGCT
CAGACTGCATGCTTTCGCCTTTGGATTCCTAGATTTCAGATTAAGGTTTAGTCAGGCTAT
TGAATAGCCCTTCAATTCTAAGTGCTGATGTGAATATCATGCAAATATGATGTACATATT
CCCATGTGCTGAGTAAGTAGATGTAGCATTTGCTAATGTTGCTATACATTTAGCATCTAA

10536   TACCAATCCGTATAAACATAAAGAAACCATACATGCATGTGGGGATCCTAACACCAGAAA
TGACTCTGAATGCAAAAAAAAAAAAAAAAAAAAAAGGGAATTTTCGTGCCCCATCCTTAG
CTTTCTCTGCTTTCTCTATTATATATGCAACTGCCTGCCCCTCTATCTTACAAAGTACTT
CGTAATCTAATGCACAGGATCAGCAGTAATGCAGCTCAGACTGCATGCTTTCGCCTTTGG
ATTCCTAGATTTCAGATTAAGGTTTAGTCAGGCTATTGAATAGCCCTTCAATTCTAAGTG
[T,C]
TGATGTGAATATCATGCAAATATGATGTACATATTCCCATGTGCTGAGTAAGTAGATGTA
GCATTTGCTAATGTTGCTATACATTTAGCATCTAAGTTATGAACCAGATTCTACCACTGG
GTAACATTAAAAAAAAGTTAGGGACTTCAGGTATGTAAAATATAGCAAATTCTATTTCTA
CGACTTTAAAGGGTATGTGTAGAGTTCTGAAAAGAATTTCTCAGCCTCCCCCAAATCCAC
ATACTTTTGGAAAGCTGATGATTGAAAAGATTAATGTGATCCTTTATTGTAACATCTAAC

11548   ACCATTGATTCTTGTTTGGAGAACATTTTGATATATTGCTTATTGGTTTTTGAGGTTGCA
TCTTTTGGGCTTATAATTTCTATATGATGTTTATTTACATGTTTGAGACTCCAGCATGGA
ATTATATGACAAAAATATTTTAGTCATTAAAACAATCTCTTTAACAAGGCTATTTTATCT
TTGATTGTAGGGTCTTTGATTTATGAAAAATTAGGAGAAAAGGCATTTGGATGGCCGGGA
AAAATTGGAGCTTTTGTTTCCATTACAATGCAGAACATTGGAGGTAAGGGGATATACTTT
[T,C]
CAATGGATCCCATAAACTTTCTATAGCGTGTTCAATAAATAAGAAAACTTATGGCAATAA
ACAGGCACTTTAGATACAGAAAAATTGCTACTTATAGTTCTTAAATTTTAAAATGATAGT
TTCTTAAATAGGTTTGTGTCCTGCTTTAATTAAAAACAGCAATATCTAAGAATGAAATAA
CATATAAAACCCTGCCAATTGAATTCTAGAATTAAAATATAAAATAAAAGCTTTCTTGAT
TTTTAATGTTATTATAGCATGAATTATTACTCTTAAAAATTGAAGAATTTGTGCTTATAT

11917   TTTAGATACAGAAAAATTGCTACTTATAGTTCTTAAATTTTAAAATGATAGTTTCTTAAA
TAGGTTTGTGTCCTGCTTTAATTAAAAACAGCAATATCTAAGAATGAAATAACATATAAA

FIGURE 3, page 14 of 23

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        ACCCTGCCAATTGAATTCTAGAATTAAAATATAAAATAAAAGCTTTCTTGATTTTTAATG
        TTATTATAGCATGAATTATTACTCTTAAAAATTGAAGAATTTGTGCTTATATCTGTCATT
        GACAAAACAGTTGACGTTTTCTATGTGTGACTGAGTTCGATTTACTAAACTGAAAAGTGG
        [G,T]
        TGTCTGGGGGAACATAGCCAAATGCTGTGGTCCTTGAAACGCAGCCTGCACTGAGCCAGC
        CCACTAGACAGTGTCTCTGGAAGTTTACTAAGGCAAAAGTCTGGCTAGGCATCAAATGCA
        CTATAAACCCCGGTTTGTTGATTCTATGGATTCTTATAATTCCCACTGAATTATCATTTC
        CAGTGTAGGACCTAGAAATATATATATATATTTTTAACAATGTTCTCTCGTTGGTGTGTT
        TGCCCACCAGCTTCATACTGTTTCTGTTGTGTCTTTGGCCCTCAGAAGGCATCCAAACCC

12840   GACTATTGCAGTAGTCTTCTAACTGGTCTTCCTGGCTTGAGTTTCCCCTGCTCTCAGATA
        AACTCTAATTTGTTCTCCAGATAAACTTTCTCAAATTTGAGTCTGTTTCTACTTTTGTCG
        TGCATAAAATTCTTCAGCATGCCTTTATTATTTTCAAGGAAAAACTTAAACTCATTGGAC
        TGACACAAGATCTTCGTCTAGTTCTTCTGCTCAATCTTTCTAAACTTTCCTAGCAATGCC
        CATATCTATCTATCTTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATC
        [T,-]
        ATCATCTATCAATTTATCCATCATCTATACCCTACATGTCCTGTGTCAAACCATAACAAA
        TTATATTTATTCCCCTAACAGTACTATTTTAATATTTTTAAAAATCATCCATGCCTTCTT
        TTCACAGGCTACTTTCTCCCCTTGACTGTCTCTCAAAGTCCTCCAACCCTAACACACACG
        CACACACACACACACACACACACACACACACATTTTCTCTCTCACTCTGCTCAC
        CTGGTCTATTGCTCCTCTAGACTGGTAAATACTAGTTCCTCTGGGCTCTCATGGTCCTGT

12844   ATTGCAGTAGTCTTCTAACTGGTCTTCCTGGCTTGAGTTTCCCCTGCTCTCAGATAAACT
        CTAATTTGTTCTCCAGATAAACTTTCTCAAATTTGAGTCTGTTTCTACTTTTGTCGTGCA
        TAAAATTCTTCAGCATGCCTTTATTATTTTCAAGGAAAAACTTAAACTCATTGGACTGAC
        ACAAGATCTTCGTCTAGTTCTTCTGCTCAATCTTTCTAAACTTTCCTAGCAATGCCCATA
        TCTATCTATCTTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATC
        [A,-]
        TCTATCAATTTATCCATCATCTATACCCTACATGTCCTGTGTCAAACCATAACAAATTAT
        ATTTATTCCCCTAACAGTACTATTTTAATATTTTTAAAAATCATCCATGCCTTCTTTTCA
        CAGGCTACTTTCTCCCCTTGACTGTCTCTCAAAGTCCTCCAACCCTAACACACACGCACA
        CACACACACACACACACACACACACACACATTTTCTCTCTCACTCTGCTCACCTGG
        TCTATTGCTCCTCTAGACTGGTAAATACTAGTTCCTCTGGGCTCTCATGGTCCTGTTTGT

12847   GCAGTAGTCTTCTAACTGGTCTTCCTGGCTTGAGTTTCCCCTGCTCTCAGATAAACTCTA
        ATTTGTTCTCCAGATAAACTTTCTCAAATTTGAGTCTGTTTCTACTTTTGTCGTGCATAA
        AATTCTTCAGCATGCCTTTATTATTTTCAAGGAAAAACTTAAACTCATTGGACTGACACA
        AGATCTTCGTCTAGTTCTTCTGCTCAATCTTTCTAAACTTTCCTAGCAATGCCCATATCT
        ATCTATCTTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCATC
        [T,-]
        ATCAATTTATCCATCATCTATACCCTACATGTCCTGTGTCAAACCATAACAAATTATATT
        TATTCCCCTAACAGTACTATTTTAATATTTTTAAAAATCATCCATGCCTTCTTTTCACAG
        GCTACTTTCTCCCCTTGACTGTCTCTCAAAGTCCTCCAACCCTAACACACACGCACACAC
        ACACACACACACACACACACACACACATTTTCTCTCTCACTCTGCTCACCTGGTCT
        ATTGCTCCTCTAGACTGGTAAATACTAGTTCCTCTGGGCTCTCATGGTCCTGTTTGTATC

13019   CTGACACAAGATCTTCGTCTAGTTCTTCTGCTCAATCTTTCTAAACTTTCCTAGCAATGC
        CCATATCTATCTATCTTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT
        CTATCATCTATCAATTTATCCATCATCTATACCCTACATGTCCTGTGTCAAACCATAACA
        AATTATATTTATTCCCCTAACAGTACTATTTTAATATTTTTAAAAATCATCCATGCCTTC
        TTTTCACAGGCTACTTTCTCCCCTTGACTGTCTCTCAAAGTCCTCCAACCCTAACACACA
        [C,-]
        GCACACACACACACACACACACACACACACACACACATTTTCTCTCTCACTCTGCTCA
        CCTGGTCTATTGCTCCTCTAGACTGGTAAATACTAGTTCCTCTGGGCTCTCATGGTCCTG
        TTTGTATCTAGTATGTTACTGTTTTCTAAAGGATATTTAAAACACTTGAGTAGAGAATA
        AGCTTTTGGAGTCTGATGGACCTGAATTTGAGTCTGTTTCTGTCACTATCTGTGAACTTG
        GGAAGATCACTGTACTCCTTTGTCTGATTTTTTCATGTATAAAAATTACCTTACAAAGGC

13022   ACACAAGATCTTCGTCTAGTTCTTCTGCTCAATCTTTCTAAACTTTCCTAGCAATGCCCA
        TATCTATCTATCTTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA
        TCATCTATCAATTTATCCATCATCTATACCCTACATGTCCTGTGTCAAACCATAACAAAT
        TATATTTATTCCCCTAACAGTACTATTTTAATATTTTTAAAAATCATCCATGCCTTCTTT
        TCACAGGCTACTTTCTCCCCTTGACTGTCTCTCAAAGTCCTCCAACCCTAACACACACGC
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FIGURE 3, page 15 of 23

[A,G]
CACACACACACACACACACACACACACACACACATTTTCTCTCTCACTCTGCTCACCT
GGTCTATTGCTCCTCTAGACTGGTAAATACTAGTTCCTCTGGGCTCTCATGGTCCTGTTT
GTATCTAGTATGTTACTGTTTTCTAAAGGATATTTTAAAACACTTGAGTAGAGAATAAGC
TTTTGGAGTCTGATGGACCTGAATTTGAGTCTGTTTCTGTCACTATCTGTGAACTTGGGA
AGATCACTGTACTCCTTTGTCTGATTTTTTCATGTATAAAAATTACCTTACAAAGGCTAT

13285   ACTGTCTCTCAAAGTCCTCCAACCCTAACACACACGCACACACACACACACACACACACA
CACACACACACACATTTTCTCTCTCACTCTGCTCACCTGGTCTATTGCTCCTCTAGACTG
GTAAATACTAGTTCCTCTGGGCTCTCATGGTCCTGTTTGTATCTAGTATGTTACTGTTTT
CTAAAGGATATTTTAAAACACTTGAGTAGAGAATAAGCTTTTGGAGTCTGATGGACCTGA
ATTTGAGTCTGTTTCTGTCACTATCTGTGAACTTGGGAAGATCACTGTACTCCTTTGTCT
[G,A]
ATTTTTTCATGTATAAAAATTACCTTACAAAGGCTATTGTGAGGATGAAATAAGGTAACA
TATGGCACATAATAAGTGTTCTGTATATGCTTCTCTCCTCCCTGGTTCTCTGCTTCCATA
TCCATGTCTCTGGAGTTGCCTGAATTATTTTTTAAATAGGCATTTAAAAAATTATAAAAC
AAATATATGATGATTGTGAAAAACTAAAACACTGCATAAATATATAAATTACCAAGAAAA
GTTTATGTCAGTCATCCTCAGAAATAACTACTCATAGGTTTTCCCCTATGCCTAATTCAA

14461   TATCGAGCATTTCATAGGATTGCCTTATAGTTGGTCTAATTTAACAACTGAAATAACCAG
GCATAAGCATAATTAACCCTGGACTCAAGAAGTTGAGTGGCAGCACCTCAGCTGTGGTTC
AAAGCATAGCCACTACTACGCTTCTAAACAATGGAATAAAGTATAAAGCGGTCTCTCAGT
CAAGCCTCACACAGGTAAGAGGCGTGACTTTAAGGGAGTAAGATGAAATATCGTAACATC
ACCCCAGAAATAATGCTCTCACTTTGGTTACTTTATTTGATTAGTTGATATTTGGCATAA
[G,C]
AGAAATCACTTGTATTTCTCTATTTAACAACTCTACATTTAGAACACTTAATTTTCTCAA
TCCCCTAAAAAAATTAACATTTACTGCAGATGTTTTCACATTAACAGATTAATGTCTGGAT
CATTCTGAATTTTTGAAGACCAAACATGTTAACATCACTGACATCACTGAAAACCAGCAA
TTAATAGCTGTAACATTGAATGGTACCTCACCAAGCCAGCTAATCAGAAATATCTCCTGT
GTTCACACTCTGTAAGATTTAGCTTTAGCCAAGGTCTTTGCAAAGATTAACCAAATAATG

15464   TGAGTTCTATTTTTAACTGAATCTTTTGGCCATGTGTCAACAAATTAACGTTATCCTTCA
CCAAATGGGTGGGCTTGAAAAAGGCGTGATGCATAAATATTTACAGTTGTAGGCAAAATT
GTAATGTTATGTATATGAATACATATTCATTTTTTCAGGGAGAAGGCTTGTAGATTTCAT
CAAGAAATCTTTCACAAGAGTAGATAATCATTCATGTATCACTTACCTAGATGCTCATGA
AATTTTGCCACTTTATATAATTCCTTAGTTAGCCAAAAGGAGAGTAAGATGAAGAGGGGG
[-,G]
AAAAAAAAAACTTCTTTGACAAAGATGGAGAGAAGCTGTCATCTCTTGTATTCTTTTATC
AATCCAGGAAGCCTTTGGTTTTGACAATAAGTGGTCTGAGACTTTGTGTACTCCTCAGAT
AGGTCCCGGAGGACTAGATTGGTGCCCATCTGCAGAAAACCAGAGGGGATATATTGACTC
TGCAGATCTGCCCTTTGATTCTGCCATCTCTCAGCTGGCCCATGCCTTTTGTTGCCAGAC
TACTGCCCAAGTTATAGACACTAACACAGGCACACTGAGTATGGGCTATGTTGATTTATA

15469   TCTATTTTTAACTGAATCTTTTGGCCATGTGTCAACAAATTAACGTTATCCTTCACCAAA
TGGGTGGGCTTGAAAAAGGCGTGATGCATAAATATTTACAGTTGTAGGCAAAATTGTAAT
GTTATGTATATGAATACATATTCATTTTTTCAGGGAGAAGGCTTGTAGATTTCATCAAGA
AATCTTTCACAAGAGTAGATAATCATTCATGTATCACTTACCTAGATGCTCATGAAATTT
TGCCACTTTATATAATTCCTTAGTTAGCCAAAAGGAGAGTAAGATGAAGAGGGGGGAAAA
[-,A]
AAAAACTTCTTTGACAAAGATGGAGAGAAGCTGTCATCTCTTGTATTCTTTTATCAATCC
AGGAAGCCTTTGGTTTTGACAATAAGTGGTCTGAGACTTTGTGTACTCCTCAGATAGGTC
CCGGAGGACTAGATTGGTGCCCATCTGCAGAAAACCAGAGGGGATATATTGACTCTGCAG
ATCTGCCCTTTGATTCTGCCATCTCTCAGCTGGCCCATGCCTTTTGTTGCCAGACTACTG
CCCAAGTTATAGACACTAACACAGGCACACTGAGTATGGGCTATGTTGATTTATAACTAA

15545   AGGCGTGATGCATAAATATTTACAGTTGTAGGCAAAATTGTAATGTTATGTATATGAATA
CATATTCATTTTTTCAGGGAGAAGGCTTGTAGATTTCATCAAGAAATCTTTCACAAGAGT
AGATAATCATTCATGTATCACTTACCTAGATGCTCATGAAATTTTGCCACTTTATATAAT
TCCTTAGTTAGCCAAAAGGAGAGTAAGATGAAGAGGGGGGAAAAAAAAAAACTTCTTTGAC
AAAGATGGAGAGAAGCTGTCATCTCTTGTATTCTTTTATCAATCCAGGAAGCCTTTGGTT
[T,C]
TGACAATAAGTGGTCTGAGACTTTGTGTACTCCTCAGATAGGTCCCGGAGGACTAGATTG
GTGCCCATCTGCAGAAAACCAGAGGGGATATATTGACTCTGCAGATCTGCCCTTTGATTC

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        TGCCATCTCTCAGCTGGCCCATGCCTTTTGTTGCCAGACTACTGCCCAAGTTATAGACAC
        TAACACAGGCACACTGAGTATGGGCTATGTTGATTTATAACTAATGAGGGCAGAACCTTA
        GAACTGCAGCTTCACTGTAAACTTTGGAGCAGGATTTAACACAGAATCAGCCCTGATACT

16199   AGAACTTGGAAGCAGTGCCAAATACACAATGACTTTTTTTTTCCATTTGGGGGATTAGATG
        TTCATCTTACATATCCCAAATGTCATAACTTGCTTGCATGTGACTTCAGTACTGTCCACA
        CCATTAAGCTGTCACATTTTCCATTTTAGCAATGTCAAGCTACCTCTTTATCATTAAATA
        TGAACTACCTGAAGTAATCAGAGCATTCATGGGACTTGAAGAAAATACTGGGTATGTCTT
        ATGCTCCCTCTGTGACATCAAGTGACTCATTCTACTTGGTCTTTTCTGATTCTAATATCC
        [T,C]
        TGTCTCTCACTTCTAGAGAATGGTACCTCAATGGCAACTACCTCATCATATTTGTGTCTG
        TTGGAATTATTCTTCCACTTTCGCTCCTTAAAAATTTAGGTAAAGATATTTTCTAACTGG
        AAATATTTTTATTTTTATTTCACATTTAAATAGGTTAGCTAATTGTAGATGCCATATTCA
        CCTTCCAAAATGCTTCTTCTAACTTCTAGGTTATCTTGGCTATACCAGTGGATTTTCTCT
        TACCTGCATGGTGTTTTTTGTTAGTGTGGTAAGTGATGTGATGACATGATCCTTGCAGGT

16798   GTTGGTTAGCATGAGTTTTTTTGTGCCTAAATTAGTGTCCTCATTTTGTTCAAGCACTTC
        ACTAATATGAAATAGTTCTTGTATCACAAGTGATTTTCTTGTAGACTAATTTAGAGCAAA
        AAAAGAGCAGCTACGATTTAAAGATAGTTGAGGTAGAATATCAAAGCTACTACTAATGGT
        TTGGTCTAGGCACACTGGTTATATATGGGGAAAAAAGGAAAACTTCAAGCAGGAACATGA
        CAATAATCTGGCATTTAGAACAGCAGAGGAGAGTCCCAGATGAGAAACAAGAAGGCTATA
        [T,C]
        CCATATTCACATGAATCAGCCATTCTCTCTTACACATTCCACCCATTAAGAGAGGACAAG
        AACAGTGGGATTAAAGAAGAAATCCTCCTCTCTAGGCCCCTGACAAAAGAGGGAATTTCT
        TGCACTATCATGAATGCCAAAATTTATAAAGCATTTCCCCAAAGAGGTAAAGGAGAAGGA
        AAAAAAGTTTTGAAGACCCATGTCACCTTAGTTTGAAGAAATAAGGAAATGATCATCTTT
        CTCATGGAAGGGCATGAAAGAGGGTGGGAAGGATTCTTGCAAAATATTGTCCTGTTAACT

18103   CATTTTTAGCATTCTAATTTGCTTTGAAATTCTGCTCATATGTTCAAAGATTCTTTAACAG
        GAAACACAGTTTATAGCTTCCTCTTCAGAGAAAATATGTACTCCATCCACTCCTCAGTAA
        CATGCTTTAATCAGAAAGGTGGGAATCAGCCCACCACAGCACTACCTTATCTTCTTTCTC
        TCCTTTCTCTCCACCATAATGGTTCAGGGGAGGGGTTCATGGCAGGTGGACAAGGAGTCG
        ATGGTTGTAATAATTTTGGCAGGTGTTGGGAATTTAAATTTGAATTTTGTTCGGAAGAAA
        [C,T]
        GATGTCAGCTGGACTAGAAATGAAAACACCCATGACGACCAAAACTTATGGTTAGGGGCA
        GCCTCGATAAGCCAGTGATGTCATTTATAGTCAGCACCTAACCCTTGTCTAGAACACATT
        CATTACAAGAGATGTGTCAATATCTGTCCTTTGTTGTCTTATTTGTACAATAGAGTCACT
        GGCTAGAAAATCTTGTTTCTTCCAGCTGATGGTCTATGGTTCATTTGTATTCTTTTCCCT
        TTGAAGTTGTTGATATTTGCTTGGGAACAAAGGATATGAACTCATTATAGCTGTTTTCCT

18421   AAATGAAAACACCCATGACGACCAAAACTTATGGTTAGGGGCAGCCTCGATAAGCCAGTG
        ATGTCATTTATAGTCAGCACCTAACCCTTGTCTAGAACACATTCATTACAAGAGATGTGT
        CAATATCTGTCCTTTGTTGTCTTATTTGTACAATAGAGTCACTGGCTAGAAAATCTTGTT
        TCTTCCAGCTGATGGTCTATGGTTCATTTGTATTCTTTTCCCTTTGAAGTTGTTGATATT
        TGCTTGGGAACAAAGGATATGAACTCATTATAGCTGTTTTCCTCTTTCCTTTAAGGGAGG
        [A,G]
        TATTATATAATAATTCTCAACTTCTTTAATCTAGACATCAGTAACCTCAGTCTTCATTCT
        CACTAAATAGCAAAACTTTCCCCATAAATTCTGATTTACCTCATAAAAAATTTCAGAACA
        CTTTCAAGTATTTTGATGTCTTTGATTTACTTTGAAAATTACATGTAGCAGTTACTCCAG
        AAGCCTGACAATTGATCTTTGGCAGCCAGGTTCCTTCTAGAATGGTTTTCAGAAGCTTTT
        CAGGTAGTCTGGACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGGTTCTTTTCCTCAT

18528   ACAAGAGATGTGTCAATATCTGTCCTTTGTTGTCTTATTTGTACAATAGAGTCACTGGCT
        AGAAAATCTTGTTTCTTCCAGCTGATGGTCTATGGTTCATTTGTATTCTTTTCCCTTTGA
        AGTTGTTGATATTTGCTTGGGAACAAAGGATATGAACTCATTATAGCTGTTTTCCTCTTT
        CCTTTAAGGGAGGATATTATATAATAATTCTCAACTTCTTTAATCTAGACATCAGTAACC
        TCAGTCTTCATTCTCACTAAATAGCAAAACTTTCCCCATAAATTCTGATTTACCTCATAA
        [G,A]
        AAATTTCAGAACACTTTCAAGTATTTTGATGTCTTTGATTTACTTTGAAAATTACATGTA
        GCAGTTACTCCAGAAGCCTGACAATTGATCTTTGGCAGCCAGGTTCCTTCTAGAATGGTT
        TTCAGAAGCTTTTCAGGTAGTCTGGACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGG
        TTCTTTTCCTCATTTAAAGTCATCTCATTATGAAATGCAAAAGCTTTCTATGTTAGGAGC
        CTGTTTCATCTTTATGTTAATTATATTCTTATTCAGTGGGCAAGCTTACTGACCTACGTG
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18722   TATTATATAATAATTCTCAACTTCTTTAATCTAGACATCAGTAACCTCAGTCTTCATTCT
CACTAAATAGCAAAACTTTCCCCATAAATTCTGATTTACCTCATAAAAAATTTCAGAACA
CTTTCAAGTATTTTGATGTCTTTGATTTACTTTGAAAATTACATGTAGCAGTTACTCCAG
AAGCCTGACAATTGATCTTTGGCAGCCAGGTTCCTTCTAGAATGGTTTTCAGAAGCTTTT
CAGGTAGTCTGGACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGGTTCTTTTCCTCAT
[T,C]
TAAAGTCATCTCATTATGAAATGCAAAAGCTTTCTATGTTAGGAGCCTGTTTCATCTTTA
TGTTAATTATATTCTTATTCAGTGGGCAAGCTTACTGACCTACGTGAAATAGACTGTTCC
TCTTCTAGGGAAATGATTGTTTTTAAGACTGAAGGACTAGTGTTTAAGAAAAATGGAAAT
GAATCCTCATTAGCTCTCTAAGACAAATTTAAATCAGCTATAAGTTTATGTACTAAATAT
GTCTTCATGATTAGCAATATAGATATACTTTTTTATTATTATTTTCATTTTGAAAAGTGA

18775   TCATTCTCACTAAATAGCAAAACTTTCCCCATAAATTCTGATTTACCTCATAAAAAATTT
CAGAACACTTTCAAGTATTTTGATGTCTTTGATTTACTTTGAAAATTACATGTAGCAGTT
ACTCCAGAAGCCTGACAATTGATCTTTGGCAGCCAGGTTCCTTCTAGAATGGTTTTCAGA
AGCTTTTCAGGTAGTCTGGACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGGTTCTTT
TCCTCATTTAAAGTCATCTCATTATGAAATGCAAAAGCTTTCTATGTTAGGAGCCTGTTT
[C,G]
ATCTTTATGTTAATTATATTCTTATTCAGTGGGCAAGCTTACTGACCTACGTGAAATAGA
CTGTTCCTCTTCTAGGGAAATGATTGTTTTTAAGACTGAAGGACTAGTGTTTAAGAAAAA
TGGAAATGAATCCTCATTAGCTCTCTAAGACAAATTTAAATCAGCTATAAGTTTATGTAC
TAAATATGTCTTCATGATTAGCAATATAGATATACTTTTTTATTATTATTTTCATTTTGA
AAAGTGATTTTTTTTTGTAAGTTTAAAAAACAAAGCTTGGTGTTCTTTCTTTTTCCAGTC

18951   CAGAAGCTTTTCAGGTAGTCTGGACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGGTT
CTTTTCCTCATTTAAAGTCATCTCATTATGAAATGCAAAAGCTTTCTATGTTAGGAGCCT
GTTTCATCTTTATGTTAATTATATTCTTATTCAGTGGGCAAGCTTACTGACCTACGTGAA
ATAGACTGTTCCTCTTCTAGGGAAATGATTGTTTTTAAGACTGAAGGACTAGTGTTTAAG
AAAAATGGAAATGAATCCTCATTAGCTCTCTAAGACAAATTTAAATCAGCTATAAGTTTA
[T,C]
GTACTAAATATGTCTTCATGATTAGCAATATAGATATACTTTTTTATTATTATTTTCATT
TTGAAAAGTGATTTTTTTTTTGTAAGTTTAAAAAACAAAGCTTGGTGTTCTTTCTTTTTCC
AGTCGGTCCCGGAGAAAAATGCAAACGGTGTCAAATATTTCCATCACGGGGATGCTTGTC
ATGTACCTGCTTGCCGCCCTCTTTGGTTACCTAACCTTCTATGGTAGGTCACTCTGAAAG
TCATTCTCTATATGCAAATCCTTGTTAGGCTGGTCCTTGACCTGGGTAGGTATGATTTTT

18974   ACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGGTTCTTTTCCTCATTTAAAGTCATCT
CATTATGAAATGCAAAAGCTTTCTATGTTAGGAGCCTGTTTCATCTTTATGTTAATTATA
TTCTTATTCAGTGGGCAAGCTTACTGACCTACGTGAAATAGACTGTTCCTCTTCTAGGGA
AATGATTGTTTTTAAGACTGAAGGACTAGTGTTTAAGAAAAATGGAAATGAATCCTCATT
AGCTCTCTAAGACAAATTTAAATCAGCTATAAGTTTATGTACTAAATATGTCTTCATGAT
[T,G]
AGCAATATAGATATACTTTTTTATTATTATTTTCATTTTGAAAAGTGATTTTTTTTTGTA
AGTTTAAAAAACAAAGCTTGGTGTTCTTTCTTTTTCCAGTCGGTCCCGGAGAAAAATGCA
AACGGTGTCAAATATTTCCATCACGGGGATGCTTGTCATGTACCTGCTTGCCGCCCTCTT
TGGTTACCTAACCTTCTATGGTAGGTCACTCTGAAAGTCATTCTCTATATGCAAATCCTT
GTTAGGCTGGTCCTTGACCTGGGTAGGTATGATTTTTAAAAATTGCCTTCTATAAGCATG

19540   GGTATGATTTTTAAAAATTGCCTTCTATAAGCATGCTCTATAGATGACACATATTCAATT
AATATACTATTTTAGTTTTGTCACTTGACCTGAGGAAATGGGGCCTGATTCAGCCTGGCT
AACAAGTTACAAGAATTTGTGAATTAACACCTATTTTATAAAAAATATCCCTCAAACAAA
ATTATTTTCCTCTAGGGATAGATGATATTTCTCTGGCTAGACTCCATAGTCCAACTCAGG
CTACAAGTGATGAGAATGAATCCACTTGCATGTGATAAAGCTCCTTTGATGGAATTATTA
[A,C]
CTGCCACACAAATAGCAGGGAAACTGCCAGGTCCTCAAGTTTGAATTTGCCTCCTCTTTA
CCAGTCAAGTCAAATCTGGGAGCTTGGGACTTTAGGTAAAATTTCTGACATATCCCATTC
TATTTTGTTATACTAAATGATTTCCTAAGAAAGAGGACATGACAGAATTCCTTCAATCT
AAGAATGCACCACCAAAAAAAAGTGACTATGGCCACATTAGATTATGCCTGCAACATTTC
CTCTCTGGCATCTTAACAGTTCACAAAGGGAGTAGGATTGTACTCCTTCCATGAAGTGTG

19841   CTGCCACACAAATAGCAGGGAAACTGCCAGGTCCTCAAGTTTGAATTTGCCTCCTCTTTA
CCAGTCAAGTCAAATCTGGGAGCTTGGGACTTTAGGTAAAATTTCTGACATATCCCATTC

TATTTTGTTATACTAAATGATTTCCTAAGAAAGAGGACATGACAGAATTTCCTTCAATCT
AAGAATGCACCACCAAAAAAAAGTGACTATGGCCACATTAGATTATGCCTGCAACATTTC
CTCTCTGGCATCTTAACAGTTCACAAAGGGAGTAGGATTGTACTCCTTCCATGAAGTGTG
[G,A]
CCACATAAACAGATTTCATGGAATCACATATTGACCTGGTAGCATATGTTTACATGAATC
AGTGTATCAATATAAATATATTTTTGTATAAACCTCCTTTTAAAGTTTTTAACTTAATTT
TTTTCTTACTGACTTGGTAAATTGAATTGCATGTATGACAAATTGTGGAGGAAAAGATTC
AGGAGTAGGCCACCATTTGCTTAGGTTTTTTTTCTATTTGACTAATATTTGACTATTAAC
CAAACATGTGCTTTAGATTGGGCATTAACTTTTTGCCGGTTGTGAAATAATGAATGACGA

20170   TATTGACCTGGTAGCATATGTTTACATGAATCAGTGTATCAATATAAATATATTTTTGTA
TAAACCTCCTTTTAAAGTTTTTAACTTAATTTTTTTCTTACTGACTTGGTAAATTGAATT
GCATGTATGACAAATTGTGGAGGAAAAGATTCAGGAGTAGGCCACCATTTGCTTAGGTTT
TTTTTCTATTTGACTAATATTTGACTATTAACCAAACATGTGCTTTAGATTGGGCATTAA
CTTTTTGCCGGTTGTGAAATAATGAATGACGAGGTCAATACTACTGAAGGTATTTTCACT
[A,C]
CTTTTTGTCTGATCTTGAGGTGAAAATCCAACTACGCTTGATTCCATAGATATTTTCTTG
TTATTTGTGCTTGGAGTCCTGAATGAAGGTGTTTTCAAGTAGGGCTGCATCTTCGTCTTA
GAGTAGTACCCACTGGGAGACCATCTAAAAATTATACTAATTTATCCCTGCACGTTACTT
ATACTTATTTTAATGAGTTTCATAAGACAAGCAAAAACTTGAAAGAGCCCAAAAATATCT
GTTTTAGTGTGGTGATGGAGTCATAGTTGTTGAGCTTGAAAAAATGGTAGCAATCATTCA

20343   TAGGTTTTTTTTCTATTTGACTAATATTTGACTATTAACCAAACATGTGCTTTAGATTGG
GCATTAACTTTTTGCCGGTTGTGAAATAATGAATGACGAGGTCAATACTACTGAAGGTAT
TTTCACTACTTTTTGTCTGATCTTGAGGTGAAAATCCAACTACGCTTGATTCCATAGATA
TTTTCTTGTTATTTGTGCTTGGAGTCCTGAATGAAGGTGTTTTCAAGTAGGGCTGCATCT
TCGTCTTAGAGTAGTACCCACTGGGAGACCATCTAAAAATTATACTAATTTATCCCTGCA
[T,C]
GTTACTTATACTTATTTTAATGAGTTTCATAAGACAAGCAAAAACTTGAAAGAGCCCAAA
AATATCTGTTTTAGTGTGGTGATGGAGTCATAGTTGTTGAGCTTGAAAAAATGGTAGCAA
TCATTCATCCTAGAGTTTACACACTGGGTTTGTAACCTGCATCAGGAGTGGCTGCACAGG
TAGGGACAGGGGAGGTGGTAGGCTGGGAGAGACAATATGTGGGGCTTGGGTCTCTCATCC
CCTTCAACAAGAGCACCTTGGTCTCTGTCTGATTTGTAATTGCTTCTGTACAGCGGAGAT

20519   GATATTTTCTTGTTATTTGTGCTTGGAGTCCTGAATGAAGGTGTTTTCAAGTAGGGCTGC
ATCTTCGTCTTAGAGTAGTACCCACTGGGAGACCATCTAAAAATTATACTAATTTATCCC
TGCACGTTACTTATACTTATTTTAATGAGTTTCATAAGACAAGCAAAAACTTGAAAGAGC
CCAAAAATATCTGTTTTAGTGTGGTGATGGAGTCATAGTTGTTGAGCTTGAAAAAAATGGT
AGCAATCATTCATCCTAGAGTTTACACACTGGGTTTGTAACCTGCATCAGGAGTGGCTGC
[G,A]
CAGGTAGGGACAGGGGAGGTGGTAGGCTGGGAGAGACAATATGTGGGGCTTGGGTCTCTC
ATCCCCTTCAACAAGAGCACCTTGGTCTCTGTCTGATTTGTAATTGCTTCTGTACAGCGG
AGATAGATTTATCACAATGTAAATGAGCTTGAGAGGCTCTTTATTTTGTATTATACCTTC
TGCAACGTTATCAGCTTCAGGACCTCTTTGTTCATTTGAATGAAGGTTGCATAGCTAATG
AGCTCAGAGGCAAGACCAGAGGTGCCTGGATTCCCAGGCCTAGGTCTTTTCCTCTGTTCT

20963   TGAGCTTGAGAGGCTCTTTATTTTGTATTATACCTTCTGCAACGTTATCAGCTTCAGGAC
CTCTTTGTTCATTTGAATGAAGGTTGCATAGCTAATGAGCTCAGAGGCAAGACCAGAGGT
GCCTGGATTCCCAGGCCTAGGTCTTTTCCTCTGTTCTGTGTTCTCTCTATAAAATGTTGC
CATAAGTGACCTGTGCTGATTTGACAACACCAAGCGGTTTCATTCTCTTTTTCCTGTTGT
AGGAGAAGTTGAAGATGAATTACTTCATGCCTACAGCAAAGTGTATACATTAGACATCCC
[T,C]
CTTCTCATGGTTCGCCTGGCAGTCCTTGTGGCAGTAACACTAACTGTGCCCATTGTCCTC
TTCCCAGTAAGTACATAAGACTTTGATGAAAGAAACCTACTTGACCCCATAAATTAGTAC
ATGTGTTCTACCTTCATTTTGATTTAATTATAGGGTGAGTTTGCAATTGCAATGCCTGAG
GATATTATTTTCCTATAGCATTTTGAGTCACTTAAAATTGGCCATTTAATGTGTAGATAG
AGCAAGTAGTTTCAGGTGGTATTTTTATAGTGTAGGAAAAAAATCATAAAACTTATTTTT

21840   AAACAGTTATGCTATCTATCACATATCTCTCTCACACATGGCCTCTGCCAGACTCACACC
AGGTCACCCCTCCCTGGCATTTGTCATTGGTGTCAGTTTGTTCTGAGATCCCAGAGCAGA
GCTGGTAGTGAAGATTTGGGCTGTGTGAGTTAAAACCACCACCTAAGGATAAACACAGGT
CTTCACCCTCCTGCCAGCTCCTGTTTCATAAACACTGAATTTACTCATTCATTTGAGGGG
GAAAAAAATAAGTGACACAGTAACCAGCACTGTCCTGGACATAATGTTCCATACAGGGCT

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          [G,T]
          GCATATGAAGACTATTTCTATAATGACACTGTGGTCACTTTAAATGCAGCTTGTGTGCTG
          AAATATATTTTGGCACATTCCTTTTTCATGAGTGCATGAAATCAGATCCGTACTACTATG
          GTGGCTAATATTTTACTCTTAAATCATGTCTTGCCTCTAATATATCTGAAAGTATTTCAG
          ATGACATACACATAGCTTTAGCCTAAAATCAGCTCCGTCTTGGGTACAAGACAGAAGACA
          ACTATAAACAGAAGGTATACGATAGGGTAAAATTGCCAGGCAAACAACTTCACTGAGAAA

22783     TGAGAAATAAAGCACTGATATAAATCTGACCATCAGGAACAGCAATAGTGTGTAAACATT
          AGATGCCATTAGAACCAAAATTGACCATAAGAACCAGAGTTCAGAAAAATGACTAACTGC
          TGTCCTTCATTATGTATTTCCACTCAACATTAGCATTTATGAAACATTTTGCACATTATC
          CTGTCCTCACCCTTGCAATGTTACATTTATATAATCTGTGTAAGTGCTCCACTGCCCCAC
          AGAGTCATAAGTCCCTGGGACTTGGTGATGTGCACAGTGACTGGCACAGAGGGTGAGCTC
          [C,T]
          GTCGTGCTTGGGAAGAAAAATGGTCTTCAAATGAATCTTGCCTTGTCTTGAAATGTATAA
          ACTGCCTTTTCTAGCAAAAGCATAGACACTCTTTCCCTTGGTGACATGTGCTACGAATTC
          AGCTGGGTTGAGGATCTGGGCTAAATGAACCAAACCTCCCTATACATGAAGGATACACAG
          AGATGGTGACAGAGAGTGGTCACTTCCGTGAGTGGATCTCAATCAAGTCCTCTGAAGCTA
          AATTCAATTTTTTTTCTTTACTAAAATGATAAAAGTTGTTATTGGCGCTTTTGCTTGTTT

22787     AAATAAAGCACTGATATAAATCTGACCATCAGGAACAGCAATAGTGTGTAAACATTAGAT
          GCCATTAGAACCAAAATTGACCATAAGAACCAGAGTTCAGAAAAATGACTAACTGCTGTC
          CTTCATTATGTATTTCCACTCAACATTAGCATTTATGAAACATTTTGCACATTATCCTGT
          CCTCACCCTTGCAATGTTACATTTATATAATCTGTGTAAGTGCTCCACTGCCCCACAGAG
          TCATAAGTCCCTGGGACTTGGTGATGTGCACAGTGACTGGCACAGAGGGTGAGCTCTGTC
          [G,A]
          TGCTTGGGAAGAAAAATGGTCTTCAAATGAATCTTGCCTTGTCTTGAAATGTATAAACTG
          CCTTTTCTAGCAAAAGCATAGACACTCTTTCCCTTGGTGACATGTGCTACGAATTCAGCT
          GGGTTGAGGATCTGGGCTAAATGAACCAAACCTCCCTATACATGAAGGATACACAGAGAT
          GGTGACAGAGAGTGGTCACTTCCGTGAGTGGATCTCAATCAAGTCCTCTGAAGCTAAATT
          CAATTTTTTTTCTTTACTAAAATGATAAAAGTTGTTATTGGCGCTTTTGCTTGTTTATTT

22825     CAATAGTGTGTAAACATTAGATGCCATTAGAACCAAAATTGACCATAAGAACCAGAGTTC
          AGAAAAATGACTAACTGCTGTCCTTCATTATGTATTTCCACTCAACATTAGCATTTATGA
          AACATTTTGCACATTATCCTGTCCTCACCCTTGCAATGTTACATTTATATAATCTGTGTA
          AGTGCTCCACTGCCCCACAGAGTCATAAGTCCCTGGGACTTGGTGATGTGCACAGTGACT
          GGCACAGAGGGTGAGCTCTGTCGTGCTTGGGAAGAAAAATGGTCTTCAAATGAATCTTGC
          [T,C]
          TTGTCTTGAAATGTATAAACTGCCTTTTCTAGCAAAAGCATAGACACTCTTTCCCTTGGT
          GACATGTGCTACGAATTCAGCTGGGTTGAGGATCTGGGCTAAATGAACCAAACCTCCCTA
          TACATGAAGGATACACAGAGATGGTGACAGAGAGTGGTCACTTCCGTGAGTGGATCTCAA
          TCAAGTCCTCTGAAGCTAAATTCAATTTTTTTTCTTTACTAAAATGATAAAAGTTGTTAT
          TGGCGCTTTTGCTTGTTTATTTCGTATAACTTAGGGCTCAGATTTTCAATGTGTCAAATG

22967     CCTCACCCTTGCAATGTTACATTTATATAATCTGTGTAAGTGCTCCACTGCCCCACAGAG
          TCATAAGTCCCTGGGACTTGGTGATGTGCACAGTGACTGGCACAGAGGGTGAGCTCTGTC
          GTGCTTGGGAAGAAAAATGGTCTTCAAATGAATCTTGCCTTGTCTTGAAATGTATAAACT
          GCCTTTTCTAGCAAAAGCATAGACACTCTTTCCCTTGGTGACATGTGCTACGAATTCAGC
          TGGGTTGAGGATCTGGGCTAAATGAACCAAACCTCCCTATACATGAAGGATACACAGAGA
          [A,T]
          GGTGACAGAGAGTGGTCACTTCCGTGAGTGGATCTCAATCAAGTCCTCTGAAGCTAAATT
          CAATTTTTTTTCTTTACTAAAATGATAAAAGTTGTTATTGGCGCTTTTGCTTGTTTATTT
          CGTATAACTTAGGGCTCAGATTTTCAATGTGTCAAATGCTGACTCACAGCATGGTTCTCC
          TGACAGTTTATTTCATTTAAGGAACTCTTCACCAGTAAGTTTATTTACTTGCCTTGATAT
          CTCCACACATTAATAATAAAACTAACAAAACCTAATCTGAATTAAAATCTATCAGCTTTA

23248     CATGAAGGATACACAGAGATGGTGACAGAGAGTGGTCACTTCCGTGAGTGGATCTCAATC
          AAGTCCTCTGAAGCTAAATTCAATTTTTTTTCTTTACTAAAATGATAAAAGTTGTTATTG
          GCGCTTTTGCTTGTTTATTTCGTATAACTTAGGGCTCAGATTTTCAATGTGTCAAATGCT
          GACTCACAGCATGGTTCTCCTGACAGTTTATTTCATTTAAGGAACTCTTCACCAGTAAGT
          TTATTTACTTGCCTTGATATCTCCACACATTAATAATAAAACTAACAAAACCTAATCTGA
          [A,G]
          TTAAAATCTATCAGCTTTAGGCATTATTTTGTGTTCTCCTTCTTTCAACATGGTAACTGG
          GCTCTCTTTCTTAGGAGCTTGAGAAGATATGACTGGGGTTTGTTTTTCTCTACTTCATTT
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                ATTATCTTTCTTTTTTCCAATCAGGTTAGTTTTTTCCTTTTTAGTAAAAGGTGCATAGTA
                ACTGCTTGTAGTATTTGTTGAACAAGTGAATAAATGAAATGAATTAAGGTAGTGTTTTCA
                CTAGCAGCCCAACATTTCTTTCTCTCTTAGTAGTGGGTGGGGTATCAGTTATGGAATGGC

    23764       GAAATGAATTAAGGTAGTGTTTTCACTAGCAGCCCAACATTTCTTTCTCTCTTAGTAGTG
                GGTGGGGTATCAGTTATGGAATGGCACCTCCTTCCAGAGGACTGATCATGTCATTTTCAG
                CTTATGCTTCCCTTTATGCAGTAAAGTTTCCATATTTCCATAAAGAACAAGAAACCAAAT
                AATCCTAATGGATATATAATGAACACACAGATGAAAATTTCACCTGCCATGCCTTTGAAA
                AAAGATCCCTAGCTACTTGTATTTCATCTTATAATTAAAATCAGTCTTTTCACTTATGTT
                [G,T]
                TCTTCAGATCTCCTGTTTTGAAGTGTATATAGATATCAACATAGAAATGCAGCGTATATT
                GCTATCAACTGCAGTGGAGCAGTGATTCGTAGGTTTTCCAACATCCTTGCCTTAAGCAAA
                CCTGCAAAATCAAAGTGTGAGCTACGTCTAAACAATGGGAGAGGCTTTTTTTTTTTTTTT
                AAGAGTTAGAACTAAGACTCTCACTTCCTCCTGTGCCTCCACATTTTTGACCTTCACATT
                GGGCCCCTGCATCAGAATACAGCACCCCCTAACAGGCTCCTGTTCAGGACTCTTTCTCTG

    23765       AAATGAATTAAGGTAGTGTTTTCACTAGCAGCCCAACATTTCTTTCTCTCTTAGTAGTGG
                GTGGGGTATCAGTTATGGAATGGCACCTCCTTCCAGAGGACTGATCATGTCATTTTCAGC
                TTATGCTTCCCTTTATGCAGTAAAGTTTCCATATTTCCATAAAGAACAAGAAACCAAATA
                ATCCTAATGGATATATAATGAACACACAGATGAAAATTTCACCTGCCATGCCTTTGAAAA
                AAGATCCCTAGCTACTTGTATTTCATCTTATAATTAAAATCAGTCTTTTCACTTATGTTT
                [C,T]
                CTTCAGATCTCCTGTTTTGAAGTGTATATAGATATCAACATAGAAATGCAGCGTATATTG
                CTATCAACTGCAGTGGAGCAGTGATTCGTAGGTTTTCCAACATCCTTGCCTTAAGCAAAC
                CTGCAAAATCAAAGTGTGAGCTACGTCTAAACAATGGGAGAGGCTTTTTTTTTTTTTTTA
                AGAGTTAGAACTAAGACTCTCACTTCCTCCTGTGCCTCCACATTTTTGACCTTCACATTG
                GGCCCCTGCATCAGAATACAGCACCCCCTAACAGGCTCCTGTTCAGGACTCTTTCTCTGG

    24432       GGATGGTGCTGGGGACCTCCCTGACCCACAGCATCTGACCCACATTTCCAGGTTCCTAGC
                GACTTGTGTCAGTAAAGAAAAAGGCACATAGCTAAGTGGAAGAGCAGATGAGGCTTGGTG
                GGAATCAGCCAGTGGTCTGCCCTAGCAAAGGTAAACAGAACTGCTGGGGGGCTTTTGGTCC
                TAGGCTCACTACTCAGGGAGGCACTTTAACATGGAATGACCAGCAAGTTTCCTTCCTGAT
                CTTTTCCACCACCACCACAAGCCTAGTACCTCCCTCCCTCTTTGCTCTGTTGCTCTCTTC
                [A,G]
                GGAATGCACTGGAAACCACCTTCAGTTCTGTTTGGAATTTTCCTATTCCTTATTCAGAAA
                GAGGAAGAAGCTTTTGCATTTACTCCAACCGTTCTACCTATTATTCCCATAAACTTTCTG
                TGATCTCATATCATTAGGCCAAATGTTAATCTTTCTGGGAGCCAGGAGACTGCTTTCACA
                TTCAGAGGCCCTGGACATATAGGACTGCCTCTAACTCACTCTAACTCAGCTTATTGACTT
                GAATGCACCTTTTTAACAAGTGACTAAAAAACAAACTGTGACTATTCTCTGAAAATGAGC

    24538       GATGAGGCTTGGTGGGAATCAGCCAGTGGTCTGCCCTAGCAAAGGTAAACAGAACTGCTG
                GGGGCTTTTGGTCCTAGGCTCACTACTCAGGGAGGCACTTTAACATGGAATGACCAGCAA
                GTTTCCTTCCTGATCTTTTCCACCACCACCACAAGCCTAGTACCTCCCTCCCTCTTTGCT
                CTGTTGCTCTCTTCGGGAATGCACTGGAAACCACCTTCAGTTCTGTTTGGAATTTTCCTA
                TTCCTTATTCAGAAAGAGGAAGAAGCTTTTGCATTTACTCCAACCGTTCTACCTATTATT
                [C,G]
                CCATAAACTTTCTGTGATCTCATATCATTAGGCCAAATGTTAATCTTTCTGGGAGCCAGG
                AGACTGCTTTCACATTCAGAGGCCCTGGACATATAGGACTGCCTCTAACTCACTCTAACT
                CAGCTTATTGACTTGAATGCACCTTTTTAACAAGTGACTAAAAAACAAACTGTGACTATT
                CTCTGAAAATGAGCCTATATCTCATACTTATTTATTCTGTTTAACACTGTGAAACAAATT
                AAGTCCTCTGGCACTATGTATATACCATAAAAAGCTTATTTGTAAGCCTACTAATTGGAC

    24693       CCTAGTACCTCCCTCCCTCTTTGCTCTGTTGCTCTCTTCGGGAATGCACTGGAAACCACC
                TTCAGTTCTGTTTGGAATTTTCCTATTCCTTATTCAGAAAGAGGAAGAAGCTTTTGCATT
                TACTCCAACCGTTCTACCTATTATTCCCATAAACTTTCTGTGATCTCATATCATTAGGCC
                AAATGTTAATCTTTCTGGGAGCCAGGAGACTGCTTTCACATTCAGAGGCCCTGGACATAT
                AGGACTGCCTCTAACTCACTCTAACTCAGCTTATTGACTTGAATGCACCTTTTTAACAAG
                [T,C]
                GACTAAAAAACAAACTGTGACTATTCTCTGAAAATGAGCCTATATCTCATACTTATTTAT
                TCTGTTTAACACTGTGAAACAAATTAAGTCCTCTGGCACTATGTATATACCATAAAAAGC
                TTATTTGTAAGCCTACTAATTGGACCAGTTTTGACAATATTGAATAAGCACTAATTGCAG
                ATCATAATGTAGAATTATAGGCTGCTGAGGAAAACAATATCACACCATTTGCTTTCCTCA
                GTTTCCTTTTCAGAATGAGTTTCATAATGTTCACTAATCCAATTTTTAAAATCCTTTACA
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24819   AACCGTTCTACCTATTATTCCCATAAACTTTCTGTGATCTCATATCATTAGGCCAAATGT
        TAATCTTTCTGGGAGCCAGGAGACTGCTTTCACATTCAGAGGCCCTGGACATATAGGACT
        GCCTCTAACTCACTCTAACTCAGCTTATTGACTTGAATGCACCTTTTTAACAAGTGACTA
        AAAAACAAACTGTGACTATTCTCTGAAAATGAGCCTATATCTCATACTTATTTATTCTGT
        TTAACACTGTGAAACAAATTAAGTCCTCTGGCACTATGTATATACCATAAAAAGCTTATT
        [C,T]
        GTAAGCCTACTAATTGGACCAGTTTTGACAATATTGAATAAGCACTAATTGCAGATCATA
        ATGTAGAATTATAGGCTGCTGAGGAAAACAATATCACACCATTTGCTTTCCTCAGTTTCC
        TTTTCAGAATGAGTTTCATAATGTTCACTAATCCAATTTTTAAAATCCTTTACAAAGTTA
        TTCTTAAACTATTTCCAGAGACTATCTGGTTTGTCATTCTAGAAATGAAATTGCCTTTTC
        AGCCTAAACAGATGGCCTTAATTTTTGGTGGAGTGGTATGAAAGGAATGTCACATGAGAA

25743   TATCCAGTTACAGCAGCGTAACTTGAGCAGCTGCTGCAAACTGAGGCTCTCTTGACCCTT
        CGCCTACTTATTTCAGCTGCTAAAATAGGGCTGAAATCTGTCAAGGATCCTGAAGGGAAG
        GATAAGATTCCTACTATTCAATTTAATTTAAGCTTTTATTCAGTGCCTGCTGTGTGCACA
        ACACTAAGCTAGAAAGTCTGAGGAATGTTTAGATTATTAGGTCCTGTTCCTTGCCTTTCA
        TAGATTTACAATCTATTGATAGGGAGAGCTAAAAAGGAGAGAAAGAGGAAGGAGCAAACA
        [C,T]
        AAAAACGTCAAAATTTTAAAATACCATTTTAAAATTTTATTTTAAAATGTTAAATACCAT
        GCAAAATTAAGGAAAACCTAGATTCATAAAAATTCCTTTCACAATCTTGTGTAAATCAAT
        TCAGTGCTTGCCCTTAATGTCTCATCCAGTCTGATGAGACATGTTTTGTGATCAACAAGG
        GTTTTACTATGTTTCTTAATTATGTGTCTTGCCTGTTATCTCTTTCTGACCGAGATTATT
        TTTAACAATAAATTCTGAAAACTAAGAAAGTGAAAGCATAAAATATTGTCTTATAAAATA

26044   AAAAACGTCAAAATTTTAAAATACCATTTTAAAATTTTATTTTAAAATGTTAAATACCAT
        GCAAAATTAAGGAAAACCTAGATTCATAAAAATTCCTTTCACAATCTTGTGTAAATCAAT
        TCAGTGCTTGCCCTTAATGTCTCATCCAGTCTGATGAGACATGTTTTGTGATCAACAAGG
        GTTTTACTATGTTTCTTAATTATGTGTCTTGCCTGTTATCTCTTTCTGACCGAGATTATT
        TTTAACAATAAATTCTGAAAACTAAGAAAGTGAAAGCATAAAATATTGTCTTATAAAATA
        [G,C]
        GCCAAGGAAAAAATGACACTCCATTTCAAATATCAAAAGTTAGCATCAAGACTGCACAAG
        ATGAATGTACAGTCATGTGTTGCTTACAAATGTGGACATATTCTGAGAAATGCATCTTTA
        GGCAATTTTGTCATTGTGCAAACACCATAGATTGTACTTGCAGCCTAATTGGTGGAGCCT
        ACTATACACTAAGGCTATATGGCATAGCCTAGTACTCCTAGGCTACAAACCTGTACAGCA
        TGTTACTGTACTGAATAGTGGAGGTACCTGTAACATAATGGTAAGTATTTGTGTCTCCAA

26555   AGTACTCCTAGGCTACAAACCTGTACAGCATGTTACTGTACTGAATAGTGGAGGTACCTG
        TAACATAATGGTAAGTATTTGTGTCTCCAAACGTAGAAAAGCTACTGTAAAAATACAGTA
        TTACAACCTTAGGGTATCACTGTCTTATATGTGGTCTGTTGTTGACCGAAATGACTATGC
        TTAATACCACTGAACTGTACACTTAAAAATGGTTAAGATGGTAAATTCTATGTTATGTAT
        GTTTTATAATAATAAAAAAATTGAAAAAAGCATCAACATCTTTTCTGGGAAAAAAGAAAA
        [G,A]
        GAAAGAAAATGCATTAGAGTGATGAGAATATTTGAAGTAATAGATAAAGTCAAAAACAAA
        GAAATGATCTTGCCTTTGAACTTTCTTGTTTAAGATTCGTACATCAGTGATCACACTGTT
        ATTTCCCAAACGACCCTTCAGCTGGATACGACATTTCCTGATTGCAGCTGTGCTTATTGC
        ACTTAATAATGTTCTGGTCATCCTTGTGCCAACTATAAAATACATCTTCGGATTCATAGG
        TGAGTTTCAGAAAGGCTTCAATTTGGTCAACCCAAACTCACGCCTCATTAAATGATGGAC

27886   GGTTTATTTAAAGTGTGTGCTGGCATCTCCTTTGCTAGGAACTGCTGGGTAAGACATTGA
        CCTTGCCCTGTGTTTGTCTTCTCAGGGGCTTCTTCTGCCACTATGCTGATTTTTATTCTT
        CCAGCAGTTTTTTATCTTAAACTTGTCAAGAAAGAAACTTTTAGGTCACCCCAAAAGGTC
        GGGGTAAGTAAACCTTGCAATTTCCCCCATTATTAGTTGTTCTTCCAACTACTTAGAATA
        AACTAGAAAATACACATAGTTCAGAAAAATGAATCAATGTACAAGAACCAAAAATCAAAA
        [A,C]
        TGGGCTAGAACTTTCTGGTAGCAGAGAAAGGGGACATATTTCTGAAACTCAAATGATTCT
        ACTTCAAATATCAAATATCCTGTGTTGAGTCTGTCATACATGTCAAATAGTAGTAGCCTT
        TCCCACAGACACATATGCTTCAGGCAAATAGCAGTGTCCAATACCAAGCTGCTGTTGTGC
        TATCCGTGGAAAATCATGCAAGAAGGAATTAGGCTCCCTAGCGGTGTTATGGAATAATTT
        AAATATTTTGGTCATGGTTGTTAGGTTTGCAAAGCCAAAGGAAAGATGTTGCTTTTGTTT

31884   CTTTTATGGTTAGTTTGAAAGAATCCATTGAAGATAGAAAATGAGAGAATAGAAGAAACC
        TGAGAATAGTAAAATAAAGAGCAGAGAAAATATGGGGGCAGGGAAAACATGTGAGTGCTA
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              AGGATTGATTATGAATGAACGATTAGGGGGATTGATGGATCACAGGGTAAGTATATGCTT
              AACTTTATAAGAAACTTCCACATAGTTTTCCACAGTGTTTCTACCATTTTCATTTCCACC
              CGTACTACCTACAACTTCCACTGACTCCACAGCCCTGCCAACATTTGGTGTTGTCTTTTG
              [T,C]
              ATTTTAGCCTTTCTAGTGGGTCTGAAATGGTAACTCATTGTGATTTTCATTTCTGCTTCT
              GTGACAACTAATGTTGAAAACTTTTCAAGTGTTTAATGGTCACTCATATATCTTCTTTTG
              TGAAGTGTGTATTCAAATCTTTTGCCCATTTTTAAAATTTAGGTTATGTGTTTTTATTGG
              GTATTTGTAGAAGCTCTTTAAATATGGATCCATGTCCAGATTGCCAATATATTTTCCCAG
              TCTATGGTATGGTTGCTTATTTTCCTAAAGGTGTCTTAATTACATCTTTCTGGGGCCAGG

    32229     TTTCATTTCTGCTTCTGTGACAACTAATGTTGAAAACTTTTCAAGTGTTTAATGGTCACT
              CATATATCTTCTTTTGTGAAGTGTGTATTCAAATCTTTTGCCCATTTTTAAAATTTAGGT
              TATGTGTTTTTATTGGGTATTTGTAGAAGCTCTTTAAATATGGATCCATGTCCAGATTGC
              CAATATATTTTCCCAGTCTATGGTATGGTTGCTTATTTTCCTAAAGGTGTCTTAATTACA
              TCTTTCTGGGGCCAGGTCACCATAGCTCAAAGTTTTGCAATTTATGTCTTAATGAGATAA
              [T,A]
              ATTAATCAGAGTGGTATAGTCAAAATTAAATGTTTTGATGTCCTGGGCCCATATAGGTAG
              GACTGGATCATCTAACCAAGATGCAAAAAAAAAAAAACAAAAAAACAAAAATAGTACTTG
              GAAAAACTTATTTTAAATTAAACA
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